```
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents DNA encoding a human TNF-alpha mutant protein specific for TNF
CC   -R2. Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 471 BP; 89 A; 163 C; 126 G; 93 T; 0 U; 0 Other;

  Query Match            95.6%;  Score 450.2;  DB 14;  Length 471;
  Best Local Similarity  97.2%;  Pred. No. 6.9e-83;
  Matches  458;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              |||||||||||||||||||||||||| |||| |  ||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCAGAACAGGTGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 6
AEB45447
ID   AEB45447 standard; DNA; 471 BP.
XX
AC   AEB45447;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R1 specific human TNF-alpha mutant protein DNA, SEQ ID No:31.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutant; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   P-PSDB; AEB45433.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Example 1; SEQ ID NO 31; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents DNA encoding a human TNF-alpha mutant protein specific for TNF
CC   -R1. Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 471 BP; 88 A; 167 C; 125 G; 91 T; 0 U; 0 Other;

  Query Match            95.6%;  Score 450.2;  DB 14;  Length 471;
  Best Local Similarity  97.2%;  Pred. No. 6.9e-83;
  Matches  458;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||  |||||||
```

```
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||    ||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGACGACGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
```

RESULT 7
AEB45448
ID AEB45448 standard; DNA; 471 BP.
XX
AC AEB45448;
XX
DT 22-SEP-2005 (first entry)
XX
DE TNF-R1 specific human TNF-alpha mutant protein DNA, SEQ ID No:32.
XX
KW tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW vasotropic; cerebroprotective; dermatological; immunomodulator;
KW antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW mutant; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2005066206-A1.
XX
PD 21-JUL-2005.
XX
PF 05-JAN-2005; 2005WO-JP000032.
XX
PR 06-JAN-2004; 2004JP-00001427.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (MAYU/) MAYUMI T.
PA (TSUT/) TSUTSUMI Y.
PA (NAKA/) NAKAGAWA S.
XX
PI Mayumi T, Tsutsumi Y, Nakagawa S, Ohta T;
XX
DR WPI; 2005-506850/51.
DR P-PSDB; AEB45434.
XX
PT Novel tumor necrosis factor TNF mutant protein, useful for treating
PT and/or preventing diseases such as inflammation, and other diseases
PT caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT rheumatoid arthritis, allergy.
XX
PS Example 1; SEQ ID NO 32; 34pp; Japanese.
XX
CC The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC a TNF mutant protein comprising an amino acid sequence derived from the
CC human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC N-terminus, and amino acid residues at positions 84-89 by other amino
CC acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC protein. The TNF mutant proteins are useful for treating and/or
CC preventing diseases such as inflammation, and other diseases caused by
CC overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC represents DNA encoding a human TNF-alpha mutant protein specific for TNF
CC -R1. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 471 BP; 89 A; 167 C; 124 G; 91 T; 0 U; 0 Other;

Query Match 95.2%; Score 448.6; DB 14; Length 471;
Best Local Similarity 97.0%; Pred. No. 1.5e-82;
Matches 457; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||| |    ||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCAACGACGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
```

RESULT 8
AEB45446
ID AEB45446 standard; DNA; 471 BP.
XX
AC AEB45446;
XX
DT 22-SEP-2005 (first entry)
XX
DE TNF-R1 specific human TNF-alpha mutant protein DNA, SEQ ID No:30.
XX
KW tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW vasotropic; cerebroprotective; dermatological; immunomodulator;
KW antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW mutant; gene; ds.
XX
OS Homo sapiens.

```
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   P-PSDB; AEB45432.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Example 1; SEQ ID NO 30; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents DNA encoding a human TNF-alpha mutant protein specific for TNF
CC   -R1. Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 471 BP; 89 A; 164 C; 127 G; 91 T; 0 U; 0 Other;

  Query Match            95.2%;  Score 448.6;  DB 14;  Length 471;
  Best Local Similarity  97.0%;  Pred. No. 1.5e-82;
  Matches  457;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||| |||||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||   ||| | |||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTAGGGAGACGGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 9
AAN60442
ID   AAN60442 standard; DNA; 471 BP.
XX
AC   AAN60442;
XX
DT   25-MAR-2003  (revised)
DT   07-AUG-1991  (first entry)
XX
DE   Sequence encoding tumour necrosis factor (TNF).
XX
KW   Anticancer agent; antitumour; antimalarial; tumour necrosis factor; ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .471
FT                   /*tag=  a
XX
PN   WO8603751-A.
XX
PD   03-JUL-1986.
XX
PF   19-DEC-1985;   85WO-EP000721.
XX
PR   21-DEC-1984;   84US-00684595.
PR   09-OCT-1985;   85US-00785847.
PR   09-OCT-1986;   86WO-US002133.
XX
PA   (BIOJ ) BIOGEN NV.
PA   (FIER/) FIERS W C.
PA   (ALLE/) ALLET B.
PA   (BIOJ ) BIOGEN INC.
XX
PI   Fiers WC,  Fransen LM,  Tavernier JHL,  Marmenout ALM,  Vanderheyd J;
PI   Allet B;
XX
DR   WPI; 1986-182891/28.
DR   P-PSDB; AAP60524.
XX
PT   Mammalian tumour necrosis factors - produced by culturing pro-karyotic
PT   hosts transformed with recombinant DNA.
XX
PS   Claim 8; Page 65; 93pp; English.
XX
CC   TNF-like polypeptides and compsns. are produced by the fermentation of
CC   host cells transformed with at least one DNA sequence which codes for a
CC   mammalian TNF-like polypeptide operatively linked to an expression
CC   control sequence in the transformed host. (Updated on 25-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 471 BP; 96 A; 157 C; 127 G; 91 T; 0 U; 0 Other;

  Query Match            94.9%;  Score 447;  DB 1;  Length 471;
  Best Local Similarity  96.8%;  Pred. No. 3.1e-82;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;
```

```
Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
```

RESULT 10
AAN70150
ID AAN70150 standard; DNA; 471 BP.
XX
AC AAN70150;
XX
DT 05-AUG-1992 (first entry)
XX
DE Sequence of the structural gene for tumour necrosis factor (TNF).
XX
KW Escherichia coli plasmid; expression vector; tumour necrosis factor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .471
FT /*tag= a
XX
PN EP220482-A.
XX
PD 06-MAY-1987.
XX
PF 19-SEP-1986; 86EP-00112941.
XX
PR 30-SEP-1985; 85JP-00217740.
XX
PA (SUNR) SUNTORY LTD.
XX
PI Oshima T, Tanaka S, Matsukura S;
XX
DR WPI; 1987-124161/18.
DR P-PSDB; AAP70095.
XX
PT New plasmid for efficient tumour necrosis factor prodn. - comprises
PT plasmid with DNA fragment having phage-gene derived promoter region and E
PT coli derived transcription termination sequence.
XX
PS Claim 7; Page 18; 31pp; English.
XX
CC The inventors claim a new plasmid for efficient tumour necrosis factor
CC prodn. . The plasmid contains a phage gene derived promoter region and E.
CC coli derived transcription termination sequence, esp. the E. coli trp a
CC gene. The transformants may achieve a TNF activity 40-300 times as great
CC as with prior transformants, and the TNF protein may comprise at least
CC 40% of the total cellular protein in the transformant. Claimed plasmids
CC are pPL T4TNFST8, pT4TNFST8 or pT4TNFST8 rop
XX
SQ Sequence 471 BP; 96 A; 157 C; 127 G; 91 T; 0 U; 0 Other;

Query Match 94.9%; Score 447; DB 1; Length 471;
Best Local Similarity 96.8%; Pred. No. 3.1e-82;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
```

RESULT 11
AAT15405
ID AAT15405 standard; DNA; 471 BP.
XX
AC AAT15405;
XX
DT 25-MAR-2003 (revised)
DT 23-APR-1996 (first entry)
XX
DE Tumour necrosis factor expression sequence.
XX
KW Tumour necrosis factor; TNF; phage T4; phage lambda; pL promoter;
KW antitumour; anticancer; antimalarial; ss.
XX
OS Synthetic.
XX
PN US5487984-A.
XX
PD 30-JAN-1996.
XX
PF 20-DEC-1985; 85US-00811654.
XX
PR 21-DEC-1984; 84US-00684595.
PR 09-OCT-1985; 85US-00785847.
XX
PA (BIOJ) BIOGEN INC.
XX

```
PI   Allet B,  Kawashima EH;
XX
DR   WPI; 1996-105230/11.
XX
PT   Prodn. of tumour necrosis factor - using recombinant DNA encoding TNF
PT   under the control of T4 or lambda pL-T4 expression control sequences.
XX
PS   Claim 3; Col 35-36; 43pp; English.
XX
CC   Recombinant DNA molecules are characterized by DNA sequences (AAT15402-
CC   05) encoding human or mouse tumour necrosis factor operatively linked to
CC   the phage T4 expression control sequence (promoter and ribosome binding
CC   site) or to the phage lambda pL promoter linked to the T4 expression
CC   control sequence. The expression control sequences provide high-level
CC   expression of recombinant TNF in host cells, esp. Escherichia coli,
CC   allowing commercial scale prodn. of TNF for use as an antitumour,
CC   anticancer or antimalarial. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 471 BP; 96 A; 157 C; 127 G; 91 T; 0 U; 0 Other;

  Query Match             94.9%;  Score 447;  DB 2;  Length 471;
  Best Local Similarity   96.8%;  Pred. No. 3.1e-82;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 12
AEB45444
ID   AEB45444 standard; DNA; 471 BP.
XX
AC   AEB45444;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R1 specific human TNF-alpha mutant protein DNA, SEQ ID No:28.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutant; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   P-PSDB; AEB45430.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Example 1; SEQ ID NO 28; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents DNA encoding a human TNF-alpha mutant protein specific for TNF
CC   -R1. Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 471 BP; 90 A; 165 C; 125 G; 91 T; 0 U; 0 Other;

  Query Match             94.9%;  Score 447;  DB 14;  Length 471;
  Best Local Similarity   96.8%;  Pred. No. 3.1e-82;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
```

```
Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||| |||||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | |||||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||   ||  | ||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTAAGGACACGGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
```

RESULT 13
AAN60441
ID AAN60441 standard; DNA; 474 BP.
XX
AC AAN60441;
XX
DT 25-MAR-2003 (revised)
DT 07-AUG-1991 (first entry)
XX
DE Sequence encoding tumour necrosis factor (TNF).
XX
KW Anticancer agent; antitumour; antimalarial; tumour necrosis factor; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1. .474
FT /*tag= a
XX
PN WO8603751-A.
XX
PD 03-JUL-1986.
XX
PF 19-DEC-1985; 85WO-EP000721.
XX
PR 21-DEC-1984; 84US-00684595.
PR 09-OCT-1985; 85US-00785847.
PR 09-OCT-1986; 86WO-US002133.
XX
PA (BIOJ) BIOGEN NV.
PA (FIER/) FIERS W C.
PA (ALLE/) ALLET B.
PA (BIOJ) BIOGEN INC.
XX
PI Fiers WC, Fransen LM, Tavernier JHL, Marmenout ALM, Vanderheyd J;
PI Allet B;
XX
DR WPI; 1986-182891/28.
DR P-PSDB; AAP60525.
XX
PT Mammalian tumour necrosis factors - produced by culturing pro-karyotic
PT hosts transformed with recombinant DNA.
XX
PS Claim 8; Page 65; 93pp; English.
XX
CC TNF-like polypeptides and compsns. are produced by the fermentation of
CC host cells transformed with at least one DNA sequence which codes for a
CC mammalian TNF-like polypeptide operatively linked to an expression
CC control sequence in the transformed host. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 474 BP; 97 A; 157 C; 128 G; 92 T; 0 U; 0 Other;

Query Match 94.9%; Score 447; DB 1; Length 474;
Best Local Similarity 96.8%; Pred. No. 3.1e-82;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          4 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 63

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 123

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 183

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 243

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||
Db        244 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 303

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        304 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 363

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        364 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 423

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 474
```

RESULT 14
AAT15404
ID AAT15404 standard; DNA; 474 BP.
XX
AC AAT15404;
XX
DT 25-MAR-2003 (revised)
DT 23-APR-1996 (first entry)
XX
DE Tumour necrosis factor expression sequence.
XX
KW Tumour necrosis factor; TNF; phage T4; phage lambda; pL promoter;
KW antitumour; anticancer; antimalarial; ss.
XX
OS Synthetic.
XX
PN US5487984-A.
XX
PD 30-JAN-1996.
XX
PF 20-DEC-1985; 85US-00811654.
XX
PR 21-DEC-1984; 84US-00684595.
PR 09-OCT-1985; 85US-00785847.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Allet B, Kawashima EH;
XX
DR WPI; 1996-105230/11.
XX
PT Prodn. of tumour necrosis factor - using recombinant DNA encoding TNF
PT under the control of T4 or lambda pL-T4 expression control sequences.
XX
PS Claim 3; Col 35; 43pp; English.

```
XX
CC   Recombinant DNA molecules are characterized by DNA sequences (AAT15402-
CC   05) encoding human or mouse tumour necrosis factor operatively linked to
CC   the phage T4 expression control sequence (promoter and ribosome binding
CC   site) or to the phage lambda pL promoter linked to the T4 expression
CC   control sequence. The expression control sequences provide high-level
CC   expression of recombinant TNF in host cells, esp. Escherichia coli,
CC   allowing commercial scale prodn. of TNF for use as an antitumour,
CC   anticancer or antimalarial. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 474 BP; 97 A; 157 C; 128 G; 92 T; 0 U; 0 Other;

  Query Match             94.9%;  Score 447;  DB 2;  Length 474;
  Best Local Similarity   96.8%;  Pred. No. 3.1e-82;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          4 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 63

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 123

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 183

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 243

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||
Db        244 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 303

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        304 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 363

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        364 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 423

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 474


RESULT 15
ADA00718
ID   ADA00718 standard; DNA; 522 BP.
XX
AC   ADA00718;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human TNF alpha related fusion protein encoding DNA SEQ ID NO:31.
XX
KW   mutein; human neutrophil gelatinase-associated lipocalin; hNGAL;
KW   rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin;
KW   24p3; mutagenesis; fusion protein; cytostatic; gene therapy;
KW   tumour imaging; cancer therapy; ds; gene.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .516
FT                   /*tag= a
FT                   /product= "tumour necrosis factor alpha and affinity tag
FT                   fusion protein"
XX
PN   WO2003029463-A2.
XX
PD   10-APR-2003.
XX
PF   18-SEP-2002; 2002WO-EP010490.
XX
PR   27-SEP-2001; 2001WO-EP011213.
PR   16-APR-2002; 2002WO-EP004223.
XX
PA   (PIER-) PIERIS PROTEOLAB AG.
XX
PI   Skerra A,  Schlehuber S;
XX
DR   WPI; 2003-372000/35.
DR   P-PSDB; ADA00722.
XX
PT   Generating a mutein of a protein, e.g. human neutrophil gelatinase-
PT   associated lipocalin, rat alpha2-microglobulin-related protein or mouse
PT   24p3/uterocalin, comprises subjecting the protein to mutagenesis.
XX
PS   Example 16; Page 116-117; 122pp; English.
XX
CC   The present invention describes a method for generating a mutein of a
CC   protein selected from a human neutrophil gelatinase-associated lipocalin
CC   (hNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse
CC   24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
CC   given target, comprising subjecting the protein to mutagenesis at
CC   positions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in
CC   muteins of the protein. Also described: (1) a mutein of hNGAL, A2m or
CC   24p3 having detectable binding affinity to a given target, obtained by
CC   the method described above; (2) a fusion protein comprising the mutein of
CC   hNGAL, A2m or 24p3, where an enzyme, a protein or a protein domain, a
CC   peptide, a signal sequence and/or an affinity tag is operably fused to
CC   the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule
CC   comprising a sequence encoding the mutein of hNGAL, A2m or 24p3 or the
CC   fusion protein of (2); and (4) a pharmaceutical composition comprising
CC   the mutein of hNGAL, A2m or 24p3 or the fusion protein described above,
CC   and a carrier. The muteins have cytostatic activity, and can be used in
CC   gene therapy. The method is useful in generating or producing a mutein of
CC   hNGAL, A2m or 24p3 or a fusion protein. The mutein of hNGAL, A2m or 24p3
CC   or the fusion protein is useful in detecting a given target by contacting
CC   the mutein with a sample suspected of containing the given target under
CC   conditions that allow complex formation between the mutein and the given
CC   target, and determining the complexed mutein by a suitable signal. The
CC   given target is a protein or protein domain, a peptide, a nucleic acid
CC   molecule, an organic molecule or a metal complex and the detection is
CC   carried out for validation of the protein as a pharmacological drug
CC   target. The mutein may also be used in medicine, e.g. for tumour imaging
CC   or directly for cancer therapy. The present sequence encodes an human
CC   tumour necrosis factor alpha and affinity tag fusion protein given in the
CC   exemplification of the present invention.
XX
SQ   Sequence 522 BP; 110 A; 170 C; 141 G; 101 T; 0 U; 0 Other;

  Query Match             94.9%;  Score 447;  DB 8;  Length 522;
  Best Local Similarity   96.8%;  Pred. No. 3.1e-82;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        103 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 162

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        163 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 222

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Search completed: September 17, 2006, 22:24:27
Job time : 710 secs

OM nucleic - nucleic search, using sw model

Run on: September 19, 2006, 08:44:47 ; Search time 3379 Seconds
(without alignments)
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Perfect score: 471
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	469.4	99.7	471	2	DD191388	DD191388 TNF antag
2	467.8	99.3	471	2	DD191389	DD191389 TNF antag
3	456.6	96.9	471	2	AX928247	AX928247 Sequence
4	456.6	96.9	471	2	DD191387	DD191387 TNF antag
5	450.2	95.6	471	2	DD191400	DD191400 TNF antag
6	450.2	95.6	471	2	DD191406	DD191406 TNF antag
7	448.6	95.2	471	2	DD191399	DD191399 TNF antag
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9	447	94.9	471	2	DD191397	DD191397 TNF antag
10	447	94.9	471	2	E01153	E01153 cDNA encodi
11	447	94.9	471	2	I02498	I02498 Sequence 2
12	447	94.9	471	2	I08410	I08410 Sequence 4
13	447	94.9	474	2	I08409	I08409 Sequence 3
14	447	94.9	522	2	AX743530	AX743530 Sequence
15	447	94.9	660	2	AR362738	AR362738 Sequence
16	447	94.9	662	2	I07549	I07549 Sequence 27
17	447	94.9	699	2	AR062128	AR062128 Sequence
18	447	94.9	699	2	AR068319	AR068319 Sequence
19	447	94.9	699	2	AR092903	AR092903 Sequence
20	447	94.9	699	2	AR178381	AR178381 Sequence
21	447	94.9	699	2	AR350050	AR350050 Sequence
22	447	94.9	699	2	AR361371	AR361371 Sequence
23	447	94.9	699	2	AR364728	AR364728 Sequence
24	447	94.9	702	2	CQ730903	CQ730903 Sequence
25	447	94.9	702	2	CS081473	CS081473 Sequence
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27	447	94.9	702	2	DD160189	DD160189 Method of
28	447	94.9	702	2	DD170851	DD170851 Method of
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ALIGNMENTS

RESULT 1
DD191388
LOCUS DD191388 471 bp DNA linear PAT 19-JAN-2006
DEFINITION TNF antagonist and TNF inhibitor containing it as an effective ingredient.
ACCESSION DD191388
VERSION DD191388.1 GI:85654774
KEYWORDS WO 2005066206-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 471)
AUTHORS Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
TITLE TNF antagonist and TNF inhibitor containing it as an effective ingredient
JOURNAL Patent: WO 2005066206-A 2 21-JUL-2005;
KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo Tsutsumi, Shinsaku Nakagawa
COMMENT OS Artificial Sequence
PN WO 2005066206-A/2
PD 21-JUL-2005
PF 05-JAN-2005 WO 2005JP000032
PR 06-JAN-2004 JP 200 4-001427
PI tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
CC
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .471
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 99.7%; Score 469.4; DB 2; Length 471;
Best Local Similarity 99.8%; Pred. No. 1.3e-110;
Matches 470; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Qy         121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Qy         421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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DD191389
LOCUS DD191389 471 bp DNA linear PAT 19-JAN-2006
DEFINITION TNF antagonist and TNF inhibitor containing it as an effective ingredient.
ACCESSION DD191389
VERSION DD191389.1 GI:85654775
KEYWORDS WO 2005066206-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 471)
AUTHORS Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
TITLE TNF antagonist and TNF inhibitor containing it as an effective ingredient
JOURNAL Patent: WO 2005066206-A 3 21-JUL-2005;
KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo Tsutsumi, Shinsaku Nakagawa
COMMENT OS Artificial Sequence
PN WO 2005066206-A/3
PD 21-JUL-2005
PF 05-JAN-2005 WO 2005JP000032
PR 06-JAN-2004 JP 200 4-001427
PI tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
CC
FH Key Location/Qualifiers.
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source 1. .471
/organism="synthetic construct"
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ORIGIN

Query Match 99.3%; Score 467.8; DB 2; Length 471;
Best Local Similarity 99.6%; Pred. No. 3.4e-110;
Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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RESULT 3
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LOCUS AX928247 471 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 12 from Patent EP1354893.
ACCESSION AX928247
VERSION AX928247.1 GI:40251445
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ikegami,H.K.
TITLE Physiologically active complex
JOURNAL Patent: EP 1354893-A 12 22-OCT-2003;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP); Mayumi, Tadanori (JP) ; Tsutsumi, Yasuo (JP) ; Nakagawa, Shinsaku (JP)
FEATURES Location/Qualifiers
source 1. .471
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DNA encoding a variant protein of human tumor necrosis factor"
ORIGIN

Query Match 96.9%; Score 456.6; DB 2; Length 471;
Best Local Similarity 98.1%; Pred. No. 2.7e-107;
Matches 462; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy         121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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DEFINITION  TNF antagonist and TNF inhibitor containing it as an effective
            ingredient.
ACCESSION   DD191387
VERSION     DD191387.1  GI:85654773
KEYWORDS    WO 2005066206-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
  TITLE     TNF antagonist and TNF inhibitor containing it as an effective
            ingredient
  JOURNAL   Patent: WO 2005066206-A 1 21-JUL-2005;
            KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo
            Tsutsumi, Shinsaku Nakagawa
COMMENT     OS   Artificial Sequence
            PN   WO 2005066206-A/1
            PD   21-JUL-2005
            PF   05-JAN-2005 WO 2005JP000032
            PR   06-JAN-2004 JP 200 4-001427
            PI   tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
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ORIGIN

  Query Match            96.9%;  Score 456.6;  DB 2;  Length 471;
  Best Local Similarity  98.1%;  Pred. No. 2.7e-107;
  Matches  462;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

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Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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RESULT 5
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LOCUS       DD191400                471 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  TNF antagonist and TNF inhibitor containing it as an effective
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ACCESSION   DD191400
VERSION     DD191400.1  GI:85654786
KEYWORDS    WO 2005066206-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
  TITLE     TNF antagonist and TNF inhibitor containing it as an effective
            ingredient
  JOURNAL   Patent: WO 2005066206-A 14 21-JUL-2005;
            KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo
            Tsutsumi, Shinsaku Nakagawa
COMMENT     OS   Artificial Sequence
            PN   WO 2005066206-A/14
            PD   21-JUL-2005
            PF   05-JAN-2005 WO 2005JP000032
            PR   06-JAN-2004 JP 200 4-001427
            PI   tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
            CC   Clone No.13
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match            95.6%;  Score 450.2;  DB 2;  Length 471;
  Best Local Similarity  97.2%;  Pred. No. 1.2e-105;
  Matches  458;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||| |||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        421 TATCTCGACTTTGCCGACGACGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 6
DD191406
LOCUS       DD191406                471 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  TNF antagonist and TNF inhibitor containing it as an effective
            ingredient.
ACCESSION   DD191406
VERSION     DD191406.1  GI:85654792
KEYWORDS    WO 2005066206-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
  TITLE     TNF antagonist and TNF inhibitor containing it as an effective
            ingredient
  JOURNAL   Patent: WO 2005066206-A 20 21-JUL-2005;
            KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo
            Tsutsumi, Shinsaku Nakagawa
COMMENT     OS   Artificial Sequence
            PN   WO 2005066206-A/20
            PD   21-JUL-2005
            PF   05-JAN-2005 WO 2005JP000032
            PR   06-JAN-2004 JP 200 4-001427
            PI   tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
            CC   Clone No.1
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             95.6%;  Score 450.2;  DB 2;  Length 471;
  Best Local Similarity   97.2%;  Pred. No. 1.2e-105;
  Matches  458;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              |||||||||||||||||||||||| |||| | ||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCAGAACAGGTGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||| ||||||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||    ||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 7
DD191399
LOCUS       DD191399                471 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  TNF antagonist and TNF inhibitor containing it as an effective
            ingredient.
ACCESSION   DD191399
VERSION     DD191399.1  GI:85654785
KEYWORDS    WO 2005066206-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
  TITLE     TNF antagonist and TNF inhibitor containing it as an effective
            ingredient
  JOURNAL   Patent: WO 2005066206-A 13 21-JUL-2005;
            KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo
            Tsutsumi, Shinsaku Nakagawa
COMMENT     OS   Artificial Sequence
            PN   WO 2005066206-A/13
            PD   21-JUL-2005
            PF   05-JAN-2005 WO 2005JP000032
            PR   06-JAN-2004 JP 200 4-001427
            PI   tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
            CC   Clone No.12
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             95.2%;  Score 448.6;  DB 2;  Length 471;
  Best Local Similarity   97.0%;  Pred. No. 3.2e-105;
  Matches  457;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||| ||||||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||    ||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        421 TATCTCGACTTTAGGGAGACGGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 8
DD191401
LOCUS       DD191401                471 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  TNF antagonist and TNF inhibitor containing it as an effective
            ingredient.
ACCESSION   DD191401
VERSION     DD191401.1  GI:85654787
KEYWORDS    WO 2005066206-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
  TITLE     TNF antagonist and TNF inhibitor containing it as an effective
            ingredient
  JOURNAL   Patent: WO 2005066206-A 15 21-JUL-2005;
            KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo
            Tsutsumi, Shinsaku Nakagawa
COMMENT     OS   Artificial Sequence
            PN   WO 2005066206-A/15
            PD   21-JUL-2005
            PF   05-JAN-2005 WO 2005JP000032
            PR   06-JAN-2004 JP 200 4-001427
            PI   tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
            CC   Clone No.14
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             95.2%;  Score 448.6;  DB 2;  Length 471;
  Best Local Similarity   97.0%;  Pred. No. 3.2e-105;
  Matches  457;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||| ||||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              ||||||||||||||| |    ||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCAACGACGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 9
DD191397
LOCUS       DD191397                471 bp    DNA     linear   PAT 19-JAN-2006
DEFINITION  TNF antagonist and TNF inhibitor containing it as an effective
            ingredient.
ACCESSION   DD191397
VERSION     DD191397.1  GI:85654783
KEYWORDS    WO 2005066206-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Mayumi,T., Tsutsumi,Y., Nakagawa,S. and Ota,T.
  TITLE     TNF antagonist and TNF inhibitor containing it as an effective
            ingredient
  JOURNAL   Patent: WO 2005066206-A 11 21-JUL-2005;
            KK Hayashibara Seibutsu Kagaku Kenkyujo,Tadanori Mayumi, Yasuo
            Tsutsumi, Shinsaku Nakagawa
COMMENT     OS   Artificial Sequence
            PN   WO 2005066206-A/11
            PD   21-JUL-2005
            PF   05-JAN-2005 WO 2005JP000032
            PR   06-JAN-2004 JP 200 4-001427
            PI   tadanori mayumi,yasuo tsutsumi,shinsaku nakagawa,tsunetaka ota
            CC   Clone No.10
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             94.9%;  Score 447;  DB 2;  Length 471;
  Best Local Similarity   96.8%;  Pred. No. 8.3e-105;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||| |||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        421 TATCTCGACTTTAAGGACACGGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 10
E01153
LOCUS       E01153                  471 bp    RNA     linear   PAT 29-SEP-1997
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DEFINITION  cDNA encoding human TNF.
ACCESSION   E01153
VERSION     E01153.1  GI:2169412
KEYWORDS    JP 1987077324-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Oshima,T., Tanaka,M. and Matsukura,S.
  TITLE     NOVEL PLASMA AND UTILIZATION THEREOF
  JOURNAL   Patent: JP 1987077324-A 1 09-APR-1987;
            SUNTORY LTD
COMMENT     OS   human
            PN   JP 1987077324-A/1
            PD   09-APR-1987
            PF   30-SEP-1985 JP 1985217740
            PI   OSHIMA TAKEHIRO, TANAKA MASAHARU, MATSUKURA SEIICHI PC
            A61K35/12,A61K35/74,A61K37/04,C07H21/04,C07K17/10,C12N15/00, PC
            C12P21/00;
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: cell_type=macrophage.
FEATURES              Location/Qualifiers
     source           1. .471
                      /organism="Homo sapiens"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             94.9%;  Score 447;  DB 2;  Length 471;
  Best Local Similarity   96.8%;  Pred. No. 8.3e-105;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||||    ||||||||||||||||||||    ||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 11
I02498
LOCUS       I02498                  471 bp ss-DNA     linear   PAT 21-MAY-1993
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DEFINITION  Sequence 2 from Patent US 4871663.
ACCESSION   I02498
VERSION     I02498.1  GI:270461
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Oshima,T., Tanaka,S. and Matsukura,S.
  TITLE     Exporession vector for human TnF
  JOURNAL   Patent: US 4871663-A 2 03-OCT-1989;
            Suntory Limited; Osaka;
            JP;
FEATURES              Location/Qualifiers
     source           1. .471
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             94.9%;  Score 447;  DB 2;  Length 471;
  Best Local Similarity   96.8%;  Pred. No. 8.3e-105;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        361 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 12
I08410
LOCUS       I08410                  471 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 4 from Patent WO 8603751.
ACCESSION   I08410
VERSION     I08410.1  GI:588881
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Fiers,W.C., Fransen,L.M., Tavernier,J.H.L., Marmenout,A.L.M., Van
            Der Heyden,J., Allet,B. and Kawashima,E.H.
  TITLE     PURIFICATION, PRODUCTION AND USE OF TUMOR NECROSIS FACTORS
  JOURNAL   Patent: WO 8603751-A 4 03-JUL-1986;
FEATURES              Location/Qualifiers
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ORIGIN

  Query Match             94.9%;  Score 447;  DB 2;  Length 471;
  Best Local Similarity   96.8%;  Pred. No. 8.3e-105;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        361 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 13
I08409
LOCUS       I08409                  474 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 3 from Patent WO 8603751.
ACCESSION   I08409
VERSION     I08409.1  GI:588880
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   Fiers,W.C., Fransen,L.M., Tavernier,J.H.L., Marmenout,A.L.M., Van
            Der Heyden,J., Allet,B. and Kawashima,E.H.
  TITLE     PURIFICATION, PRODUCTION AND USE OF TUMOR NECROSIS FACTORS
  JOURNAL   Patent: WO 8603751-A 3 03-JUL-1986;
FEATURES             Location/Qualifiers
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  Query Match             94.9%;  Score 447;  DB 2;  Length 474;
  Best Local Similarity   96.8%;  Pred. No. 8.3e-105;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        124 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 183

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        304 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 363

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        364 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 423

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        424 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 474


RESULT 14
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LOCUS       AX743530                522 bp    DNA     linear   PAT 12-MAY-2003
DEFINITION  Sequence 31 from Patent WO03029463.
ACCESSION   AX743530
VERSION     AX743530.1  GI:30577288
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Skerra,A. and Schlehuber,S.
  TITLE     Muteins of human neutrophil gelatinase-associated lipocalin and
            related proteins
  JOURNAL   Patent: WO 03029463-A 31 10-APR-2003;
            Pieris ProteoLab AG (DE)
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ORIGIN

  Query Match             94.9%;  Score 447;  DB 2;  Length 522;
  Best Local Similarity   96.8%;  Pred. No. 8.4e-105;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;
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Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        163 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 222

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        223 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 282

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        403 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 462

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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RESULT 15
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LOCUS AR362738 660 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 1 from patent US 5182196.
ACCESSION AR362738
VERSION AR362738.1 GI:34423123
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 660)
AUTHORS Allet,B. and Kawashima,E.H.
TITLE Expression systems for overproduction of desired proteins
JOURNAL Patent: US 5182196-A 1 26-JAN-1993;
Biogen, Inc.; Cambridge, MA;
EPX;
FEATURES Location/Qualifiers
source 1. .660
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ORIGIN

Query Match 94.9%; Score 447; DB 2; Length 660;
Best Local Similarity 96.8%; Pred. No. 8.6e-105;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db        203 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 262

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        263 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 322

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        323 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 382

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        563 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 613
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Job time : 3382 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 16, 2006, 09:42:12 ; Search time 297 Seconds
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488.981 Million cell updates/sec

Title: US-10-668-178-3
Perfect score: 814
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	779	95.7	233	1	TNFA_HUMAN	P01375 homo sapien
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3	772	94.8	233	1	TNFA_PAPSP	P33620 papio sp. (
4	770	94.6	232	1	TNFA_PANTR	Q8hzd9 pan troglod
5	761	93.5	233	1	TNFA_MACMU	P48094 macaca mula
6	758	93.1	233	1	TNFA_MACFA	P79337 macaca fasc
7	757	93.0	233	1	TNFA_PAPHU	O77510 papio hamad
8	754	92.6	233	1	TNFA_PAPAN	P59695 papio anubi
9	744	91.4	149	2	O97543_AOTNA	O97543 aotus nancy
10	738	90.7	233	1	TNFA_CANFA	P51742 canis famil
11	732	89.9	233	2	Q2MJ87_TRIMA	Q2mj87 trichechus
12	731	89.8	233	1	TNFA_FELCA	P19101 felis silve
13	714	87.7	233	2	Q2LAH3_DICBI	Q2lah3 diceros bic
14	708	87.0	233	1	TNFA_SAISC	Q8mkg8 saimiri sci
15	702	86.2	149	2	O97538_AOTVO	O97538 aotus vocif
16	702	86.2	149	2	Q9TTG8_AOTNI	Q9ttg8 aotus nigri
17	697	85.6	234	1	TNFA_HORSE	P29553 equus cabal
18	691	84.9	217	2	Q9BEG0_CYCDI	Q9beg0 cyclopes di
19	687	84.4	217	2	Q9BEG1_BRATR	Q9beg1 bradypus tr
20	679	83.4	233	1	TNFA_DELLE	Q8wnr1 delphinapte
21	677.5	83.2	232	1	TNFA_PIG	P23563 sus scrofa
22	669	82.2	233	2	Q2LAH2_STEBR	Q2lah2 steno breda
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24	652	80.1	217	2	Q9BEF4_CABUN	Q9bef4 cabassous u
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27	638	78.4	234	2	Q53ZM5_CAPHI	Q53zm5 capra hircu
28	637.5	78.3	234	1	TNFA_CAVPO	P51435 cavia porce
29	635	78.0	216	2	Q9BEC4_TALEU	Q9bec4 talpa europ
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32	633.5	77.8	235	1	TNFA_RABIT	P04924 oryctolagus
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34	632	77.6	229	1	TNFA_CEREL	P51743 cervus elap
35	631	77.5	233	1	TNFA_BOVIN	Q06599 bos taurus
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ALIGNMENTS

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AC P01375; O43647; Q9P1Q2; Q9UIV3;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 21-FEB-2006, entry version 85.
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE necrosis factor, membrane form; Tumor necrosis factor, soluble form).
GN Name=TNF; Synonyms=TNFA, TNFSF2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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RX MEDLINE=87217060; PubMed=3555974;
RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
RA Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
RA Filippov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,
RA Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;
RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-
RT alpha) and lymphotoxin (TNF-beta) in the human genome.";
RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85086244; PubMed=6392892;
RA Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,
RA Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;
RT "Human tumour necrosis factor: precursor structure, expression and
RT homology to lymphotoxin.";
RL Nature 312:724-729(1984).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85137898; PubMed=3883195;
RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;
RT "Cloning and expression in Escherichia coli of the gene for human
RT tumour necrosis factor.";
RL Nature 313:803-806(1985).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86016093; PubMed=2995927;
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,
RA Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;
RT "Human lymphotoxin and tumor necrosis factor genes: structure,
RT homology and chromosomal localization.";
RL Nucleic Acids Res. 13:6361-6373(1985).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85142190; PubMed=3856324;
RA Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,
RA van Arsdell J.N., Yamamoto R., Mark D.F.;

RT "Molecular cloning of the complementary DNA for human tumor necrosis
RT factor.";
RL Science 228:149-154(1985).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86030296; PubMed=3932069;
RA Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,
RA Ruysschaert M.R., van Vliet A., Fiers W.;
RT "Molecular cloning and expression of human tumor necrosis factor and
RT comparison with mouse tumor necrosis factor.";
RL Eur. J. Biochem. 152:515-522(1985).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93272029; PubMed=8499947;
RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
RA Cohen D.;
RT "Dense Alu clustering and a potential new member of the NF kappa B
RT family within a 90 kilobase HLA class III segment.";
RL Nat. Genet. 3:137-145(1993).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99218514; PubMed=10202016;
RA Neville M.J., Campbell R.D.;
RT "A new member of the Ig superfamily and a V-ATPase G subunit are among
RT the predicted products of novel genes close to the TNF locus in the
RT human MHC.";
RL J. Immunol. 162:4745-4754(1999).
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656967; DOI=10.1101/gr.1736803;
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA Campbell R.D., Hood L.;
RT "Analysis of the gene-dense major histocompatibility complex class III
RT region and its comparison to mouse.";
RL Genome Res. 13:2621-2636(2003).
RN [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Shiina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN [11]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
RT "Genome diversity in HLA: a new strategy for detection of genetic
RT polymorphisms in expressed genes within the HLA class III and class I
RT regions.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN [12]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN [13]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LEU-84.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN [14]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [15]
RP NUCLEOTIDE SEQUENCE OF 77-233.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN [16]
RP NUCLEOTIDE SEQUENCE OF 84-214.
RC TISSUE=Prostatic carcinoma;
RA Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [17]
RP PHOSPHORYLATION (MEMBRANE FORM).
RX MEDLINE=96170872; PubMed=8597870;
RA Pocsik E., Duda E., Wallach D.;
RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
RT transfected HeLa cells.";
RL J. Inflamm. 45:152-160(1995).
RN [18]
RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
RX MEDLINE=99221647; PubMed=10205166; DOI=10.1093/emboj/18.8.2119;
RA Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
RA Roufogalis B.D., Chaudhri G.;
RT "A casein kinase I motif present in the cytoplasmic domain of members
RT of the tumour necrosis factor ligand family is implicated in 'reverse
RT signalling'.";
RL EMBO J. 18:2119-2126(1999).
RN [19]
RP MUTAGENESIS.
RX MEDLINE=91184128; PubMed=2009860;
RA Ostade X.V., Tavernier J., Prange T., Fiers W.;
RT "Localization of the active site of human tumour necrosis factor
RT (hTNF) by mutational analysis.";
RL EMBO J. 10:827-836(1991).
RN [20]
RP MYRISTOYLATION.
RX MEDLINE=93018820; PubMed=1402651; DOI=10.1084/jem.176.4.1053;
RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;
RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
RT specific lysine residues.";
RL J. Exp. Med. 176:1053-1062(1992).
RN [21]
RP CLEAVAGE BY ADAM17.
RX MEDLINE=97186575; PubMed=9034191; DOI=10.1038/385733a0;
RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhart W., Carter H.L.,
RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,
RA Mitchell J., Moyer M., Pahel G., Rocque W., Overton L.K., Schoenen F.,
RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
RT "Cloning of a disintegrin metalloproteinase that processes precursor
RT tumour-necrosis factor-alpha.";
RL Nature 385:733-736(1997).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=89159409; PubMed=2922050; DOI=10.1038/338225a0;
RA Jones E.Y., Stuart D.I., Walker N.P.;
RT "Structure of tumour necrosis factor.";
RL Nature 338:225-228(1989).
RN [23]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).

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RX   MEDLINE=91193276; PubMed=1964681;
RA   Jones E.Y., Stuart D.I., Walker N.P.;

  Query Match             95.7%;  Score 779;  DB 1;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 6.4e-71;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 2
Q5STB3_HUMAN
ID   Q5STB3_HUMAN    PRELIMINARY;    PRT;   233 AA.
AC   Q5STB3;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-MAR-2006, entry version 8.
DE   Tumor necrosis factor (TNF superfamily, member 2).
GN   Name=TNF; ORFNames=DAQB-87N14.5-001, DASS-280D8.2-001,
GN   XXbac-BCX270M2.1-001, XXbac-BPG296P20.12-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood leukocyte;
RA   Shiina T., Ota M., Takasu M., Katsuyama Y., Hashimoto N., Tokunaga K.,
RA   Inoko H.;
RT   "Genome diversity in HLA: A new strategy for detection of genetic
RT   polymorphisms in expressed genes within the HLA class III and class I
RT   regions.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL662847; CAI17678.1; -; Genomic_DNA.
DR   EMBL; AL662801; CAI18292.1; -; Genomic_DNA.
DR   EMBL; AL929587; CAI18649.1; -; Genomic_DNA.
DR   EMBL; BX248519; CAI41940.1; -; Genomic_DNA.
DR   EMBL; AB202113; BAE78639.1; -; Genomic_DNA.
DR   SMR; Q5STB3; 82-233.
DR   Ensembl; ENSG00000111956; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   233 AA;  25644 MW;  3DF90F96C9031FFE CRC64;

  Query Match             95.7%;  Score 779;  DB 2;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 6.4e-71;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 3
TNFA_PAPSP
ID   TNFA_PAPSP     STANDARD;      PRT;   233 AA.
AC   P33620;
DT   01-FEB-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 1.
DT   07-FEB-2006, entry version 40.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio sp. (Baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=61183;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Sanjanwala M., Edwards A.;
RL   Submitted (SEP-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X62141; CAA44068.1; -; Genomic_DNA.
DR   PIR; S22052; S22052.
DR   HSSP; P01375; 1A8M.
DR   SMR; P33620; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
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DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034443.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034444.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25557 MW;  455360B48DC74173 CRC64;

  Query Match             94.8%;  Score 772;  DB 1;  Length 233;
  Best Local Similarity   95.5%;  Pred. No. 3.3e-70;
  Matches  150;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:|||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 4
TNFA_PANTR
ID   TNFA_PANTR     STANDARD;      PRT;   232 AA.
AC   Q8HZD9;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 2.
DT   07-FEB-2006, entry version 30.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=22381002; PubMed=12493009;
RX   DOI=10.1034/j.1600-065X.2002.19008.x;
RA   Kulski J.K., Shiina T., Anzai T., Kohara S., Inoko H.;
RT   "Comparative genomic analysis of the MHC: the evolution of class I
RT   duplication blocks, diversity and complexity from shark to man.";
RL   Immunol. Rev. 190:95-122(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;
RA   Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA   Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA   Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA   Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT   "Comparative sequencing of human and chimpanzee MHC class I regions
RT   unveils insertions/deletions as the major path to genomic
RT   divergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 33-186.
RA   O'Huigin C., Tichy H., Klein J.;
RT   "Molecular evolution in higher primates; gene specific and organism
RT   specific characteristics.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB054536; BAB83882.1; -; Genomic_DNA.
DR   EMBL; BA000041; BAC78157.1; -; Genomic_DNA.
DR   EMBL; AY091964; AAM76582.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8HZD9; 81-232.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    232       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT                                /FTId=PRO_0000034437.
FT   CHAIN        77    232       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034438.
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     58    232       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    144    176       By similarity.
FT   CONFLICT     77     77       G -> VR (in Ref. 3).
SQ   SEQUENCE   232 AA;  25446 MW;  E4D71B19C6AE0D03 CRC64;

  Query Match             94.6%;  Score 770;  DB 1;  Length 232;
  Best Local Similarity   96.1%;  Pred. No. 5.3e-70;
  Matches  149;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 SSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 62
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Db         78 SSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 137

Qy         63 LFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGG 122
              || |||||||||||||||||||||||| |||||||:|||||||||||| ||||||||||
Db        138 LFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGG 197

Qy        123 VFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||| |||||||||||||||||||||||||||||
Db        198 VFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 232
```

```
RESULT 5
TNFA_MACMU
ID   TNFA_MACMU     STANDARD;      PRT;   233 AA.
AC   P48094; Q5TM21; Q8HZD6;
DT   01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1996, sequence version 1.
DT   07-FEB-2006, entry version 37.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15269276; DOI=10.1093/molbev/msh216;
RA   Kulski J.K., Anzai T., Shiina T., Inoko H.;
RT   "Rhesus macaque class I duplicon structures, organization, and
RT   evolution within the alpha block of the major histocompatibility
RT   complex.";
RL   Mol. Biol. Evol. 21:2079-2091(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 33-187.
RA   O'Huigin C., Tichy H., Klein J.;
RT   "Molecular evolution in higher primates; gene specific and organism
RT   specific characteristics.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U19850; AAA86712.1; -; mRNA.
DR   EMBL; AB128049; BAD69724.1; -; Genomic_DNA.
DR   EMBL; AY091967; AAM76585.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P48094; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034431.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034432.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25630 MW;  9F6F85050595FD59 CRC64;

  Query Match             93.5%;  Score 761;  DB 1;  Length 233;
  Best Local Similarity   94.3%;  Pred. No. 4.4e-69;
  Matches  148;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||| |||||||||||||||| |||||||:||||||||||||| |||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 6
TNFA_MACFA
ID   TNFA_MACFA     STANDARD;      PRT;   233 AA.
AC   P79337;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1997, sequence version 1.
DT   07-FEB-2006, entry version 36.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lymphocyte;
RA   Tatsumi M.;
RT   "Molecular cloning and expression of cynomolgus monkey TNF-alpha.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
```

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CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; AB000513; BAA19131.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P79337; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034429.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034430.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25558 MW;  6ABF2C3AB132C217 CRC64;

  Query Match             93.1%;  Score 758;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 8.9e-69;
  Matches  147;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||:|||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALVANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||| |||||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 7
TNFA_PAPHU
ID   TNFA_PAPHU     STANDARD;      PRT;   233 AA.
AC   O77510;
DT   15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1998, sequence version 1.
DT   07-FEB-2006, entry version 35.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio hamadryas ursinus (Chacma baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=36229;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=98147379; PubMed=9488055; DOI=10.1016/S0161-5890(97)00124-7;
RA   Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT   "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RT   alpha.";
RL   Mol. Immunol. 34:1041-1042(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF019963; AAC31675.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O77510; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034441.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034442.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25658 MW;  B9403255058D4A03 CRC64;

  Query Match             93.0%;  Score 757;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 1.1e-68;
  Matches  147;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| || |||||||||||||||||||||||||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVVHVVANPQAEGQLQWLNRRANALLANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||| |||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 8
TNFA_PAPAN
ID   TNFA_PAPAN     STANDARD;      PRT;   233 AA.
AC   P59695;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 1.
DT   07-FEB-2006, entry version 27.
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DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA   Villinger F.J., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY234222; AAO85335.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P59695; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT                                /FTId=PRO_0000034439.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034440.
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     58    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25736 MW;  0C477F9EB6CC9909 CRC64;

  Query Match             92.6%;  Score 754;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 2.3e-68;
  Matches  147;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||.||||||||||||||||||||||||||||  ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVEPTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||| |||||||||||||||| |||||||:|||||||||||||| ||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 9
O97543_AOTNA
ID   O97543_AOTNA   PRELIMINARY;   PRT;   149 AA.
AC   O97543;
DT   01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1999, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AF014513; AAD01539.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O97543; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16466 MW;  3C2A6140778EFA8A CRC64;

  Query Match             91.4%;  Score 744;  DB 2;  Length 149;
  Best Local Similarity   96.0%;  Pred. No. 1.4e-67;
  Matches  143;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 PSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFSGQ 67
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ 60

Qy         68 GCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
              |||||||||||||||||||| |||||||:|||||||||||| ||||||||||||||||
Db         61 GCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLE 120
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Qy        128 PGDRLSAEINRPDYLDFAESGQVYFGIIA 156
              ||||||||||||||||||||||||||||||
Db        121 KGDRLSAEINRPDYLDFAESGQVYFGIIA 149


RESULT 10
TNFA_CANFA
ID   TNFA_CANFA     STANDARD;      PRT;   233 AA.
AC   P51742; Q28339;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-FEB-2006, entry version 39.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Fiers W.;
RT   "Tumour necrosis factor.";
RL   (In) Sim E. (eds.);
RL   The natural immune system humoral factors, pp.65-119, IRL Press,
RL   Oxford (1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT   "Cloning and expression of the cDNA for canine tumor necrosis factor-
RT   alpha in E. coli.";
RL   Lymphokine Res. 13:191-196(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Wagner J.L., Palti Y., DiDario D.D.;
RT   "Genomic map of a portion of the canine MHC class I histocompatibility
RT   complex.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 74-205.
RC   STRAIN=Beagle; TISSUE=Blood;
RA   Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RT   "Expression of canine TNF, IL-1 and IL-6 mRNAs in peripheral blood
RT   monocytes and cell lines.";
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X94932; CAA64403.1; -; Genomic_DNA.
DR   EMBL; S74068; AAB32391.1; -; mRNA.
DR   EMBL; AY423389; AAR27885.1; -; Genomic_DNA.
DR   EMBL; Z70046; CAA93908.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P51742; 82-233.
DR   Ensembl; ENSCAFG00000000517; Canis familiaris.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034409.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034410.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
FT   CONFLICT     59     60       QR -> PE (in Ref. 2).
FT   CONFLICT     66     66       G -> C (in Ref. 2).
FT   CONFLICT     74     74       A -> V (in Ref. 4).
FT   CONFLICT    111    111       A -> D (in Ref. 2).
FT   CONFLICT    116    116       G -> D (in Ref. 2).
FT   CONFLICT    134    135       IY -> DS (in Ref. 2).
SQ   SEQUENCE   233 AA;  25447 MW;  7B2588FBC8B25340 CRC64;

  Query Match             90.7%;  Score 738;  DB 1;  Length 233;
  Best Local Similarity   89.8%;  Pred. No. 9.8e-67;
  Matches  141;  Conservative    7;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |:|||||||| |||||||||:||||||||:|||||||||||||| ||||:|||:|||||||
Db         77 VKSSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLIVPSDGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||| |||||| |||||||:|||||||||| || ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQRETPEGTEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |:||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPNYLDFAESGQVYFGIIAL 233


RESULT 11
Q2MJ87_TRIMA
ID   Q2MJ87_TRIMA   PRELIMINARY;   PRT;   233 AA.
AC   Q2MJ87;
DT   07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   07-FEB-2006, sequence version 1.
DT   07-FEB-2006, entry version 1.
DE   Tumor necrosis factor alpha.
OS   Trichechus manatus latirostris.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Afrotheria; Sirenia; Trichechidae; Trichechus.
OX   NCBI_TaxID=127582;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Colle C.F. III, Walsh C.J.;
RT   "Molecular cloning and functional characterization of the Florida
RT   manatee (Trichechus manatus) tumor necrosis facter alpha.";
RL   Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
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DR   EMBL; DQ333395; ABC58216.1; -; mRNA.
SQ   SEQUENCE   233 AA;  25625 MW;  475200AA9BC34665 CRC64;

  Query Match             89.9%;  Score 732;  DB 2;  Length 233;
  Best Local Similarity   90.4%;  Pred. No. 4e-66;
  Matches  142;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||| |||||||||||||||||||:||||||||||||| |||||:|||:|||||||
Db         77 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSRRANALLANGVELIDNQLMVPSDGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||| ||||| ||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCHRETPEEAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |:||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPNYLDFAESGQVYFGIIAL 233


RESULT 12
TNFA_FELCA
ID   TNFA_FELCA     STANDARD;      PRT;   233 AA.
AC   P19101; Q8HYM0;
DT   01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 2.
DT   07-FEB-2006, entry version 46.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   MEDLINE=91016860; PubMed=2216740;
RA   McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
RT   "Gene sequence of feline tumor necrosis factor alpha.";
RL   Nucleic Acids Res. 18:5563-5563(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Bone marrow;
RA   Daniel S.L., Brenner C.A., Legendre A.M., Soloman A., Rouse B.T.;
RT   "Feline cytokines TNF alpha and IL-1 beta: PCR cloning and sequencing
RT   of cDNA.";
RL   Anim. Biotechnol. 3:117-121(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 95-185.
RA   Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;
RT   "Characterization of 8 feline type I markers.";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X54000; CAA37948.1; -; Genomic_DNA.
DR   EMBL; M92061; AAA30818.1; -; mRNA.
DR   EMBL; AF459810; AAO15590.1; -; Genomic_DNA.
DR   PIR; S11688; S11688.
DR   HSSP; P01375; 4TSV.
DR   SMR; P19101; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034419.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034420.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
FT   CONFLICT     28     28       G -> R (in Ref. 2).
FT   CONFLICT    104    104       W -> R (in Ref. 1).
FT   CONFLICT    141    141       T -> K (in Ref. 3).
FT   CONFLICT    151    151       L -> H (in Ref. 2).
FT   CONFLICT    155    155       T -> A (in Ref. 1).
FT   CONFLICT    210    210       T -> A (in Ref. 2).
SQ   SEQUENCE   233 AA;  25382 MW;  03E51823A7863510 CRC64;

  Query Match             89.8%;  Score 731;  DB 1;  Length 233;
  Best Local Similarity   89.8%;  Pred. No. 5.1e-66;
  Matches  141;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||| |||||||||:||||||||:||||||||||||| |||| |||:|||||||
Db         77 LRSSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLKVPSDGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||:|||||||||||||| |||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFTGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||| ||| | ||||||||||||||||
Db        197 GGVFQLEKGDRLSTEINLPAYLDFAESGQVYFGIIAL 233


RESULT 13
Q2LAH3_DICBI
ID   Q2LAH3_DICBI   PRELIMINARY;   PRT;   233 AA.
AC   Q2LAH3;
DT   21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   21-FEB-2006, sequence version 1.
DT   21-FEB-2006, entry version 1.
DE   Tumor necrosis factor alpha.
OS   Diceros bicornis (Black rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Rhinocerotidae;
OC   Diceros.
OX   NCBI_TaxID=9805;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
```

```
RA   Colle C.F. III, Walsh C.J.;
RT   "Molecular cloning and functional characterization of the black
RT   rhinoceros (Diceros bicornis) tumor necrosis factor alpha.";
RL   Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ340435; ABC68489.1; -; mRNA.
SQ   SEQUENCE   233 AA;  25460 MW;  C42BD327A3804BC1 CRC64;

  Query Match             87.7%;  Score 714;  DB 2;  Length 233;
  Best Local Similarity   88.5%;  Pred. No. 2.8e-64;
  Matches  139;  Conservative    5;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||| ||| |||||||||||||||||: |||||||||||| ||||||| :|||||||
Db         77 LRSSSRNPSDKPVAHVVANPQAEGQLQWLSGRANALLANGVELTDNQLVVPVDGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||| |||||||||||| |||||| |||||||:|||| |||||||| ||||||||
Db        137 QVLFRGQGCSSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQTETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||:|| |||||||| ||||||||||||||||||||
Db        197 GGVFKLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 14
TNFA_SAISC
ID   TNFA_SAISC     STANDARD;      PRT;   233 AA.
AC   Q8MKG8;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
RA   Heraud J.M., Lavergne A., Kazanji M.;
RT   "Molecular cloning, characterization, and quantification of squirrel
RT   monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL   Immunogenetics 54:20-29(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22516846; PubMed=12628762; DOI=10.1016/S0165-2427(03)00018-7;
RA   Merien F., Lavergne A., Behr C., Contamin H.;
RT   "Sequencing and analysis of genomic DNA and cDNA encoding TNF-alpha in
RT   the squirrel monkey (Saimiri sciureus).";
RL   Vet. Immunol. Immunopathol. 92:37-43(2003).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF294760; AAK92047.1; -; mRNA.
DR   EMBL; AJ437697; CAD27179.1; -; Genomic_DNA.
DR   EMBL; AJ437698; CAD27180.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8MKG8; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT                                /FTId=PRO_0000034453.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034454.
FT   TOPO_DOM      1     32       Cytoplasmic (Potential).
FT   TRANSMEM     33     55       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     56    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25578 MW;  197FB066F744FCAD CRC64;

  Query Match             87.0%;  Score 708;  DB 1;  Length 233;
  Best Local Similarity   87.3%;  Pred. No. 1.1e-63;
  Matches  137;  Conservative    7;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||| ||| ||||||||||||||||||||||||||||||||||:||||:||
Db         77 VRSSSRIPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSDGLYLVYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||  ||||:|||||||||  |||||||:|||||||| ||: :||||||||
Db        137 QVLFKGQGCPSTFTLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTHPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||: || || ||||||||||||
Db        197 GGVFQLEKGDRLSAEISPPDSLDLAESGQVYFGIIAL 233


RESULT 15
O97538_AOTVO
ID   O97538_AOTVO   PRELIMINARY;   PRT;   149 AA.
AC   O97538;
DT   01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1999, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus vociferans (Spix's owl monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=57176;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
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RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF014508; AAD01534.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O97538; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16415 MW;  86F1B9BCED16E689 CRC64;

  Query Match             86.2%;  Score 702;  DB 2;  Length 149;
  Best Local Similarity   89.9%;  Pred. No. 2.6e-63;
  Matches  134;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          8 PSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFSGQ 67
              ||| |||||||||||||||||||||||||||||||||||||||||||:|||||| ||.
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLVYSQVLFKGQ 60

Qy         68 GCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
              ||||| :||||:|||||||||  |||||||:|||||||| ||: ||||||||||||||
Db         61 GCPSTFMLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTNPWYEPIYLGGVFQLE 120

Qy        128 PGDRLSAEINRPDYLDFAESGQVYFGIIA 156
               ||||||||| ||||| ||||||||||||
Db        121 KGDRLSAEINLPDYLDLAESGQVYFGIIA 149


Search completed: September 16, 2006, 09:50:17
Job time : 299 secs
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 16, 2006, 09:45:32 ; Search time 39 Seconds
(without alignments)
387.334 Million cell updates/sec

Title: US-10-668-178-3
Perfect score: 814
Sequence: 1 VRSSSRTPSDMPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	779	95.7	233	1	QWHUN	tumor necrosis fac
2	772	94.8	233	1	S22052	tumor necrosis fac
3	712	87.5	233	2	S11688	tumor necrosis fac
4	697	85.6	234	1	JQ1344	tumor necrosis fac
5	677.5	83.2	232	1	S12606	tumor necrosis fac
6	634.5	77.9	235	1	QWMSN	tumor necrosis fac
7	633.5	77.8	234	1	A25451	tumor necrosis fac
8	631	77.5	185	2	S52715	tumor necrosis fac
9	631	77.5	233	1	S24642	tumor necrosis fac
10	629	77.3	234	1	JH0529	tumor necrosis fac
11	628.5	77.2	235	2	I54490	tumor necrosis fac
12	624.5	76.7	193	2	S06192	tumor necrosis fac
13	619.5	76.1	235	2	JU0029	tumor necrosis fac
14	258.5	31.8	197	1	JH0309	tumor necrosis fac
15	250.5	30.8	204	1	S24641	lymphotoxin - bovi
16	247.5	30.4	204	1	S17289	tumor necrosis fac
17	238	29.2	202	1	JN0869	tumor necrosis fac
18	236.5	29.1	202	1	B27303	tumor necrosis fac
19	213.5	26.2	205	1	QWHUX	lymphotoxin alpha
20	173	21.3	244	2	A46066	lymphotoxin beta -
21	166.5	20.5	278	2	A49266	fas ligand - rat
22	161.5	19.8	279	2	A53062	Fas ligand - mouse
23	149	18.3	281	2	I38707	Fas ligand - human
24	143	17.6	306	2	I49139	lymphotoxin-beta -
25	129	15.8	261	2	I53476	CD40 ligand - huma
26	127	15.6	260	2	S21738	CD40 ligand - mous
27	116	14.3	261	2	S53090	CD40 ligand - bovi
28	80	9.8	1560	2	T09202	probable tail comp
29	77.5	9.5	675	2	E75393	hypothetical prote
30	77	9.5	468	2	AC3595	UDP-N-acetylglucos
31	76	9.3	286	2	E91277	probable oxidoredu
32	76	9.3	286	2	E86118	probable oxidoredu
33	74.5	9.2	403	2	I54192	aminomethyltransfe
34	74.5	9.2	479	2	F70965	hypothetical prote
35	74	9.1	286	2	S56436	hypothetical 29.7K
36	74	9.1	473	2	A47050	glutamate-ammonia
37	73.5	9.0	217	2	F86343	hypothetical prote
38	73.5	9.0	352	2	T51835	3-methyl-2-oxobuta
39	73	9.0	533	2	B83813	catalase katX [imp
40	73	9.0	1626	2	T09271	probable tail comp
41	72.5	8.9	385	2	AH2269	heterocyst specifi
42	72.5	8.9	1336	2	T17479	hypothetical prote
43	72.5	8.9	2352	2	C83229	probable non-ribos
44	72	8.8	339	2	T49597	hypothetical prote
45	72	8.8	1369	2	D86178	hypothetical prote

ALIGNMENTS

RESULT 1
QWHUN
tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrom
A;Reference number: A93585; MUID:86016093; PMID:2995927
A;Accession: A93585
A;Molecule type: DNA
A;Residues: 1-233 <NED>
A;Cross-references: UNIPROT:P01375; UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g372
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka,
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <IRI>
A;Cross-references: UNIPARC:UPI000000D745; EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.;
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to ly
A;Reference number: A93351; MUID:85086244; PMID:6392892
A;Accession: A93351
A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Cross-references: UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA266
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc
R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; V
Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
A;Accession: A44189
A;Molecule type: mRNA
A;Residues: 1-62,'S',64-233 <WAN>
A;Cross-references: UNIPARC:UPI000002FB8A; GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; And
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: B61478
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,
A;Cross-references: UNIPARC:UPI00001735C7; UNIPARC:UPI00001735C8; UNIPARC:UPI00001735C9;
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, E
Eur. J. Biochem. 152, 515-522, 1985

A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A;Reference number: I53311; MUID:86030296; PMID:3932069
A;Accession: I53311
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <MAR>
A;Cross-references: UNIPARC:UPI000000D745; GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:
A;Experimental source: U-937 cells
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
A;Accession: S62610
A;Molecule type: protein
A;Residues: 77-99 <TAK>
A;Cross-references: UNIPARC:UPI00001735CD
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regic
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
A;Cross-references: UNIPARC:UPI00001735CE; GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bring
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction
out detriment to normal cells. It can also act synergistically with interferon gamma to
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely
ut are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macr
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match 95.7%; Score 779; DB 1; Length 233;
Best Local Similarity 96.2%; Pred. No. 4.9e-72;
Matches 151; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233
```

RESULT 2
S22052
#umor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S22052
R;Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
A;Cross-references: UNIPROT:P33620; UNIPARC:UPI00001370C4; EMBL:X62141; NID:g38159; PIDN:
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

Query Match 94.8%; Score 772; DB 1; Length 233;
Best Local Similarity 95.5%; Pred. No. 2.5e-71;
Matches 150; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233
```

RESULT 3
S11688
tumor necrosis factor alpha precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11688
R;McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A;Title: Gene sequence of feline tumor necrosis factor alpha.
A;Reference number: S11688; MUID:91016860; PMID:2216740
A;Accession: S11688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MCG>
A;Cross-references: UNIPROT:P19101; UNIPARC:UPI00001370BE; EMBL:X54000; NID:g1084; PIDN:(
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

Query Match 87.5%; Score 712; DB 2; Length 233;
Best Local Similarity 88.5%; Pred. No. 3.4e-65;
Matches 139; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

```
Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||||||| |||||||||:|||||| |:||||||||||||| |||| |||:|||||||
Db         77 LRSSSRTPSDKPVAHVVANPEAEGQLQRLSRRANALLANGVELTDNQLKVPSDGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||:|||||||||||| ||| |||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFTGQGCPSTHVLLTHAISRFAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
```

```
                  ||||||| ||||| ||| | ||||||||||||||||||
Db        197 GGVFQLEKGDRLSTEINLPAYLDFAESGQVYFGIIAL 233


RESULT 4
JQ1344
tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ1344
R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: UNIPROT:P29553; UNIPARC:UPI00001370BF; GB:M64087; NID:g164244; PIDN:
C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

  Query Match             85.6%;  Score 697;  DB 1;  Length 234;
  Best Local Similarity   85.4%;  Pred. No. 1.2e-63;
  Matches  134;  Conservative   11;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||| ||||||||||||||||||: ||||||||||:| ||||||| :|||||||
Db         78 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSGRANALLANGVKLTDNQLVVPLDGLYLIYS 137

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||:|||| : |||||||:|||  |:|| ||| ||||||||
Db        138 QVLFKGQGCPSTHVLLTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPWYEPIYL 197

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||:|||||||:|:|||||||||||||||||
Db        198 GGVFQLEKGDQLSAEINQPNYLDFAESGQVYFGIIAL 234


RESULT 5
S12606
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Accession: S12606
A;Molecule type: DNA
A;Residues: 1-232 <DRE>
A;Cross-references: UNIPROT:P23563; UNIPARC:UPI00001370C6; EMBL:X54001; NID:g2135; PIDN:
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17290
A;Molecule type: DNA
A;Residues: 1-232 <KUH>
A;Cross-references: UNIPARC:UPI00001370C6; EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:
A;Note: the authors translated the codon GAG for residue 202 as Gly
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fa
A;Reference number: S18965
A;Accession: S18965
A;Molecule type: mRNA
A;Residues: 1-232 <CHO>
A;Cross-references: UNIPARC:UPI00001370C6; EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: UNIPARC:UPI000016C6F7; GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g
C;Genetics:
A;Introns: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myris
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

  Query Match             83.2%;  Score 677.5;  DB 1;  Length 232;
  Best Local Similarity   85.4%;  Pred. No. 1.1e-61;
  Matches  134;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:| || |||||||| :||||||| :  |||||||||:|:|||||||:|||||||
Db         77 LRSSSQT-SDKPVAHVVANVKAEGQLQWQSGYANALLANGVKLKDNQLVVPTDGLYLIYS 135

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||:| |||||||||||||| |||||||:||||||||||||| ||||||||
Db        136 QVLFRGQGCPSTNVFLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 195

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||| ||||||||||||||||||||
Db        196 GGVFQLEKDDRLSAEINLPDYLDFAESGQVYFGIIAL 232


RESULT 6
QWMSN
tumor necrosis factor alpha precursor - mouse
N;Alternate names: cachectin; TNF alpha
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696
R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A;Reference number: A22908; MUID:88224564; PMID:2836146
A;Accession: A22908
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
A;Cross-references: UNIPROT:P06804; UNIPARC:UPI0000022334; GB:M20155
R;Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucle
A;Reference number: S03791; MUID:87298639; PMID:3040015
A;Accession: S03791
A;Molecule type: DNA
A;Residues: 1-235 <SHA>
A;Cross-references: UNIPARC:UPI0000022334; GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g
A;Note: article in Russian with English abstract
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor nec
A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Accession: A27303
A;Molecule type: DNA
A;Residues: 1-235 <SEM>
A;Cross-references: UNIPARC:UPI0000022334; GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g
```

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R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosi
A;Reference number: A25164; MUID:85298296; PMID:3898078
A;Accession: A25164
A;Molecule type: mRNA
A;Residues: 1-235 <PEN>
A;Cross-references: UNIPARC:UPI0000022334; GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:
R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima,
Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expre
A;Reference number: A23127; MUID:85242112; PMID:2989794
A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
A;Cross-references: UNIPARC:UPI0000022334; GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g
R;Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results
A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
A;Cross-references: UNIPARC:UPI00001735CF
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region of
A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'R',232-235 <RES>
A;Cross-references: UNIPARC:UPI000016D086; GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor ne
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
A;Cross-references: UNIPARC:UPI00001735D0
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

  Query Match             77.9%;  Score 634.5;  DB 1;  Length 235;
  Best Local Similarity   75.2%;  Pred. No. 2.9e-57;
  Matches  118;  Conservative   21;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| | | ||:||::|||||||||::|:|||||||::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYS 139

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||  :||||||:|| |:|||  ||||||::||| ::|||||| ||||||||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYL 198

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||:||||:| | |||||||||||||:|||
Db        199 GGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 7
A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25454; A25451; JS0727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.;
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabb
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: UNIPROT:P04924; UNIPARC:UPI000016C5C2; GB:M12845; NID:g165759; PIDN:
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Cross-references: UNIPARC:UPI000016C5C2
A;Note: this sequence differs from that shown in having a Gln inserted between residues
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: JS0727
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62,'Q',63-234 <SHA>
A;Cross-references: UNIPARC:UPI00001370C7; GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membr
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

  Query Match             77.8%;  Score 633.5;  DB 1;  Length 234;
  Best Local Similarity   78.3%;  Pred. No. 3.7e-57;
  Matches  123;  Conservative   15;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||:||  || |:||||||| |||||||::|||||||||::| |||||||::|||||||
Db         79 LRSASRALSDKPLAHVVANPQVEGQLQWLSQRANALLANGMKLTDNQLVVPADGLYLIYS 138

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||||||| | :||||||:|| ||||   |||||||:||| ||||| ||   |||||||
Db        139 QVLFSGQGCRS-YVLLTHTVSRFAVSYPNKVNLLSAIKSPCHRETPEEAEPMAWYEPIYL 197

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||| |:|:|:||| ||||||||||||
Db        198 GGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFGIIAL 234


RESULT 8
S52715
tumor necrosis factor alpha precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C;Accession: S52715
R;Mertens, B.; Gaidulis, L.
submitted to the EMBL Data Library, March 1995
A;Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and bo
A;Reference number: S52715
A;Accession: S52715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-185 <MER>
A;Cross-references: UNIPARC:UPI000016C282; EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PI
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein
```

F;33/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;97-129/Disulfide bonds: #status predicted

Query Match 77.5%; Score 631; DB 2; Length 185;
Best Local Similarity 77.7%; Pred. No. 4.9e-57;
Matches 122; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |: |||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         29 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 88

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| ||||||| : |||||||||||||| ||:||||:||| ||||| ||| |||||||
Db         89 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 148

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |||||:||||||||||||
Db        149 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 185
```

RESULT 9
S24642
tumor necrosis factor alpha precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I46047; S24642
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46047
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <CL2>
A;Cross-references: UNIPROT:Q06599; UNIPARC:UPI00001370B8; EMBL:Z14137; NID:g796; PIDN:C
C;Genetics:
A;Gene: TNFA
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

Query Match 77.5%; Score 631; DB 1; Length 233;
Best Local Similarity 77.7%; Pred. No. 6.6e-57;
Matches 122; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

```
Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |: |||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         77 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| ||||||| : |||||||||||||| ||:||||:||| ||||| ||| |||||||
Db        137 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |||||:||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 233
```

RESULT 10
JH0529
tumor necrosis factor alpha precursor - sheep
N;Alternate names: cachectin; TNF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0529; S48118; S13114; S20661
R;Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with
A;Reference number: JH0529; MUID:92112044; PMID:1765267
A;Accession: JH0529
A;Molecule type: mRNA
A;Residues: 1-234 <GRE>
A;Cross-references: UNIPROT:P23383; UNIPARC:UPI000002CD39; EMBL:X55152; NID:g1405; PIDN:C
A;Experimental source: alveolar macrophage
R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A;Reference number: S48118; MUID:92155784; PMID:1786996
A;Accession: S48118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-234 <NAS>
A;Cross-references: UNIPARC:UPI000002CD39; EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PII
R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A;Reference number: S13114; MUID:91067496; PMID:2251151
A;Accession: S13114
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62,64-234 <YOU>
A;Cross-references: UNIPARC:UPI000016C4EC; EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g
A;Note: comparison with the introns of homologous sequences suggest that this is probably
C;Superfamily: tumor necrosis factor
C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lymphok
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Query Match 77.3%; Score 629; DB 1; Length 234;
Best Local Similarity 77.7%; Pred. No. 1.1e-56;
Matches 122; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  :: |||||||| | |||:| :  ||||:||||||:||||||::|||||||
Db         78 LRSSSQASNNKPVAHVVANISAPGQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYS 137

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| | ||||| : |||||||||||||| ||:||||:||| ||| ||||| |||||||
Db        138 QVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETLEGAEAKPWYEPIYQ 197

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |:|||:||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPEYLDYAESGQVYFGIIAL 234
```

RESULT 11
I54490
tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I54490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuco
A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cross-references: UNIPROT:P36939; UNIPARC:UPI00001370C5; GB:M59233; NID:g202506; PIDN:A
C;Genetics:
A;Gene: PlTNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 77.2%; Score 628.5; DB 2; Length 235;

```
  Best Local Similarity   75.2%;  Pred. No. 1.2e-56;
  Matches  118;  Conservative   21;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| | : ||:||:| ||||||||::|:|||||:|::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGANALLANGMDLKDNQLVIPADGLYLVYS 139

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||| |::|||||:|| ||||:  |||||||:||| :|||||:|  ||||||||
Db        140 QVLFKGQGC-SSYVLLTHTVSRFAVSYEDKVNLLSAIKSPCPKETPEGSELKPWYEPIYL 198

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||:| | ||||||||||||||:|||
Db        199 GGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 12
S06192
tumor necrosis factor alpha precursor - goat (fragment)
N;Alternate names: cachectin; TNF alpha
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S06192; S41867
R;Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989
A;Reference number: S06192
A;Accession: S06192
A;Molecule type: mRNA
A;Residues: 1-193 <GOL>
A;Cross-references: UNIPROT:P13296; UNIPARC:UPI000016C3FD; EMBL:X14828; NID:g992; PIDN:C
R;Rimstad, E.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41867
A;Accession: S41867
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'L'
A;Cross-references: UNIPARC:UPI000016C3FE; EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PI
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein
F;42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;106-138/Disulfide bonds: #status predicted

  Query Match             76.7%;  Score 624.5;  DB 2;  Length 193;
  Best Local Similarity   78.3%;  Pred. No. 2.4e-56;
  Matches  123;  Conservative   14;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |: ||||||||  | |||:| :  |||| ||||||:|||||||::||||||
Db         38 LRSSSQASSNKPVAHVVANISAPGQLRWGDSYANALKANGVELKDNQLVVPTDGLYLIYS 97

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| | ||||| : |||||||||||||| ||:||||:||| ||||| ||| |||||||
Db         98 QVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPE-AEAKPWYEPIYQ 156

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||:|:|||:||||||||||||
Db        157 GGVFQLEKGDRLSAEINQPEYLDYAESGQVYFGIIAL 193


RESULT 13
JU0029
tumor necrosis factor alpha precursor - rat
N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0029; JN0868; S21674
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis f
A;Reference number: JU0029
A;Accession: JU0029
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
A;Cross-references: UNIPROT:P16599; UNIPARC:UPI000004368F
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A;Reference number: JN0868; MUID:94040766; PMID:8224868
A;Accession: JN0868
A;Molecule type: DNA
A;Residues: 1-235 <KWO>
A;Cross-references: UNIPARC:UPI000004368F; GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g
R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitr
A;Reference number: S21674; MUID:92329007; PMID:1627266
A;Accession: S21674
A;Molecule type: mRNA
A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>
A;Cross-references: UNIPARC:UPI000017086D; GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membr
F;80-235/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

  Query Match             76.1%;  Score 619.5;  DB 2;  Length 235;
  Best Local Similarity   74.5%;  Pred. No. 9.9e-56;
  Matches  117;  Conservative   20;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| ||| ||:||::|||||||||::|:||||||::|||||||
Db         80 LRSSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLIYS 139

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||  :||||||:|| |:|||  |:|||||:||| ::|||||  |||||:||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPWYEPMYL 198

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| || ||||:| | |||  |||||||:|||
Db        199 GGVFQLEKGDLLSAEVNLPKYLDITESGQVYFGVIAL 235


RESULT 14
JH0309
tumor necrosis factor beta precursor - rabbit
N;Alternate names: lymphotoxin; TNF beta
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0309; PN0098
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-l
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: JH0309
A;Molecule type: DNA
A;Residues: 1-197 <SH2>
A;Cross-references: UNIPROT:P10154; UNIPARC:UPI00001370CE; GB:M60340; GB:M35326; NID:g165
R;Shakhov, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Nedospas
Mol. Biol. (Mosk.) 23, 1743-1750, 1989
A;Title: Cloning and structural analysis of the genes, coding for rabbit tumor necrosis f
A;Reference number: PN0098; MUID:90220566; PMID:2633043
A;Accession: PN0098
A;Molecule type: mRNA
A;Residues: 1-197 <SHA>
A;Cross-references: UNIPARC:UPI00001370CE; GB:X55745; NID:g297167; PIDN:CAA39275.1; PID:g
C;Genetics:
A;Introns: 25/3; 61/1
C;Superfamily: tumor necrosis factor
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C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-197/Product: lymphotoxin #status predicted <MAT>

  Query Match             31.8%;  Score 258.5;  DB 1;  Length 197;
  Best Local Similarity   40.0%;  Pred. No. 6.4e-19;
  Matches   60;  Conservative   21;  Mismatches   58;  Indels   11;  Gaps    4;

Qy         12 PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFSGQGCP- 70
              | ||:| :| |:  |:|      | | :|  | :| |:||| ||| :||||:|||:||
Db         55 PAAHLVGDPSAQDSLRWRANTDRAFLRHGFSLSNNSLLVPSSGLYFVYSQVVFSGEGCSP 114

Qy         71 ---STHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
                | : | | :   :  |   | |||| :| |    |:|    ||   :| | || |
Db        115 KAVPTPLYLAHEVQLFSSQYSFHVPLLSAQKSVC--PGPQG----PWVRSVYQGAVFLLT 168

Qy        128 PGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        169 QGDQLSTHTDGIAHLLLSPS-SVFFGAFAL 197


RESULT 15
S24641
lymphotoxin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I46046; S24641
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46046
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-204 <CL2>
A;Cross-references: UNIPROT:Q06600; UNIPARC:UPI00001370CA; EMBL:Z14137; NID:g796; PIDN:C
C;Genetics:
A;Introns: 32/3; 68/1
C;Superfamily: tumor necrosis factor

  Query Match             30.8%;  Score 250.5;  DB 1;  Length 204;
  Best Local Similarity   38.7%;  Pred. No. 4.4e-18;
  Matches   58;  Conservative   22;  Mismatches   59;  Indels   11;  Gaps    4;

Qy         12 PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFSGQGC-- 69
              | ||:| :|  :  |:|      | | :|  | :| |:||: ||| :||||:|||:||
Db         62 PAAHLVGDPSTQDSLRWRANTDRAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGRGCFP 121

Qy         70 --PSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
                | : | | :   :  |   | |||| :| |    |:|    ||   :| | || |
Db        122 RATPTPLYLAHEVQLFSPQYPFHVPLLSAQKSVC--PGPQG----PWVRSVYQGAVFLLT 175

Qy        128 PGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               ||:||   :   :|  : |  |:||  ||
Db        176 RGDQLSTHTDGISHLLLSPS-SVFFGAFAL 204


Search completed: September 16, 2006, 09:51:02
Job time : 41 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 16, 2006, 09:52:12 ; Search time 34 Seconds
(without alignments)
326.225 Million cell updates/sec

Title: US-10-668-178-3
Perfect score: 814
Sequence: 1 VRSSSRTPSDMPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	779	95.7	157	7	US-11-297-810-1	Sequence 1, Appli
2	779	95.7	157	7	US-11-143-926-1	Sequence 1, Appli
3	779	95.7	157	7	US-11-314-941-1	Sequence 1, Appli
4	779	95.7	170	6	US-10-490-953-35	Sequence 35, Appl
5	779	95.7	233	7	US-11-361-015-4	Sequence 4, Appli
6	779	95.7	233	7	US-11-382-837-3	Sequence 3, Appli
7	779	95.7	233	7	US-11-377-165A-3	Sequence 3, Appli
8	770	94.6	233	7	US-11-337-690-5	Sequence 5, Appli
9	748	91.9	150	7	US-11-315-825-28	Sequence 28, Appl
10	748	91.9	152	6	US-10-794-755-5	Sequence 5, Appli
11	748	91.9	152	6	US-10-527-832-6	Sequence 6, Appli
12	634.5	77.9	235	7	US-11-241-106-8	Sequence 8, Appli
13	213.5	26.2	147	6	US-10-794-755-6	Sequence 6, Appli
14	213.5	26.2	147	7	US-11-315-825-31	Sequence 31, Appl
15	213.5	26.2	205	7	US-11-382-837-4	Sequence 4, Appli
16	213.5	26.2	205	7	US-11-377-165A-4	Sequence 4, Appli
17	212	26.0	51	6	US-10-978-053C-1	Sequence 1, Appli
18	211.5	26.0	205	7	US-11-337-690-6	Sequence 6, Appli
19	173	21.3	244	7	US-11-382-837-5	Sequence 5, Appli
20	173	21.3	244	7	US-11-377-165A-5	Sequence 5, Appli
21	166.5	20.5	179	6	US-10-861-934-14	Sequence 14, Appl
22	166.5	20.5	278	6	US-10-861-934-16	Sequence 16, Appl
23	166.5	20.5	278	6	US-10-861-934-26	Sequence 26, Appl
24	161.5	19.8	137	6	US-10-861-934-10	Sequence 10, Appl
25	161.5	19.8	138	6	US-10-861-934-12	Sequence 12, Appl
26	161.5	19.8	179	6	US-10-861-934-22	Sequence 22, Appl
27	161.5	19.8	279	6	US-10-861-934-24	Sequence 24, Appl
28	161.5	19.8	279	6	US-10-861-934-32	Sequence 32, Appl
29	161.5	19.8	279	7	US-11-241-106-5	Sequence 5, Appli
30	161.5	19.8	279	7	US-11-337-690-4	Sequence 4, Appli
31	157.5	19.3	137	6	US-10-861-934-18	Sequence 18, Appl
32	157.5	19.3	138	6	US-10-861-934-20	Sequence 20, Appl
33	149	18.3	179	6	US-10-861-934-6	Sequence 6, Appli
34	149	18.3	261	7	US-11-015-117-47	Sequence 47, Appl
35	149	18.3	267	7	US-11-337-690-3	Sequence 3, Appli
36	149	18.3	276	7	US-11-015-117-49	Sequence 49, Appl
37	149	18.3	281	6	US-10-511-937-2473	Sequence 2473, Ap
38	149	18.3	281	6	US-10-861-934-8	Sequence 8, Appli
39	149	18.3	281	6	US-10-861-934-30	Sequence 30, Appl
40	149	18.3	281	7	US-11-015-117-45	Sequence 45, Appl
41	149	18.3	281	7	US-11-015-117-46	Sequence 46, Appl
42	149	18.3	281	7	US-11-382-837-6	Sequence 6, Appli
43	149	18.3	281	7	US-11-377-165A-6	Sequence 6, Appli
44	149	18.3	282	7	US-11-015-117-48	Sequence 48, Appl
45	147.5	18.1	136	6	US-10-861-934-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-11-297-810-1
; Sequence 1, Application US/11297810
; Publication No. US20060121037A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghrayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of Human
; TITLE OF INVENTION: Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-049
; CURRENT APPLICATION NUMBER: US/11/297,810
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: U.S. 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S.08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-810-1

Query Match 95.7%; Score 779; DB 7; Length 157;
Best Local Similarity 96.2%; Pred. No. 3.5e-76;
Matches 151; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 2
US-11-143-926-1
; Sequence 1, Application US/11143926
; Publication No. US20060140946A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Chimeric Antibody Fragments
;  FILE REFERENCE: 0975.1005-052
;  CURRENT APPLICATION NUMBER: US/11/143,926
;  CURRENT FILING DATE:  2005-06-02
;  PRIOR APPLICATION NUMBER: U.S. 09/897,724
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S.07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-143-926-1

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  Best Local Similarity   96.2%;  Pred. No. 3.5e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 3
US-11-314-941-1
; Sequence 1, Application US/11314941
; Publication No. US20060140949A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Human Anti-TNF Antibodies and Peptides
;  FILE REFERENCE: 0975.1005-059
;  CURRENT APPLICATION NUMBER: US/11/314,941
;  CURRENT FILING DATE:  2005-12-20
;  PRIOR APPLICATION NUMBER: U.S. 10/198,845
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S.08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-314-941-1

  Query Match             95.7%;  Score 779;  DB 7;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 3.5e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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RESULT 4
US-10-490-953-35
; Sequence 35, Application US/10490953
; Publication No. US20060088908A1
; GENERAL INFORMATION:
;  APPLICANT: SKERRA, ARNE
;  APPLICANT:  SCHLEHUBER, STEFFEN
;  TITLE OF INVENTION: MUTEINS OF HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN AND
;  TITLE OF INVENTION:  RELATED PROTEINS
;  FILE REFERENCE: 029029-0104
;  CURRENT APPLICATION NUMBER: US/10/490,953
;  CURRENT FILING DATE:  2004-03-29
;  PRIOR APPLICATION NUMBER: PCT/EP02/10490
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: PCT/EP02/04223
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/11213
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;  PRIOR FILING DATE: 2001-09-27
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: amino acid sequence
;   FEATURE:
;   NAME/KEY: CHAIN
;   LOCATION: (1)..(170)
;   OTHER INFORMATION: fusion protein of tumor necrosis factor alpha and
;   OTHER INFORMATION: affinity tag
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(13)
;   OTHER INFORMATION: Affinity tag Arg-Gly-Ser-His(6)-Gly(3)
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (14)..(170)
;   OTHER INFORMATION: mature tumor necrosis factor alpha
US-10-490-953-35

  Query Match             95.7%;  Score 779;  DB 6;  Length 170;
  Best Local Similarity   96.2%;  Pred. No. 3.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 73

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         74 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 133

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        134 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 170


RESULT 5
US-11-361-015-4
; Sequence 4, Application US/11361015
; Publication No. US20060194740A1
; GENERAL INFORMATION:
;  APPLICANT: Ulevitch, Richard J.
;  APPLICANT:  da Silva, Jean
;  APPLICANT:  Han, Jiahuai
;  APPLICANT:  The Scripps Research Institute
;  TITLE OF INVENTION: NOD1 as an Anti-tumor Agent
;  FILE REFERENCE: 1361.057US1
;  CURRENT APPLICATION NUMBER: US/11/361,015
;  CURRENT FILING DATE:  2006-02-23
;  PRIOR APPLICATION NUMBER: US 60/656,175
;  PRIOR FILING DATE: 2005-02-25
;  PRIOR APPLICATION NUMBER: US 60/752,794
;  PRIOR FILING DATE: 2005-12-22
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-361-015-4

  Query Match             95.7%;  Score 779;  DB 7;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 5.8e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 6
US-11-382-837-3
; Sequence 3, Application US/11382837
; Publication No. US20060193859A1
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Methods of Treatment Using Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C8
;  CURRENT APPLICATION NUMBER: US/11/382,837
;  CURRENT FILING DATE:  2006-05-11
;  PRIOR APPLICATION NUMBER: 09/589,288
;  PRIOR FILING DATE: 2000-06-08
;  PRIOR APPLICATION NUMBER: 09/507,968
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/122,388
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: 60/124,097
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/126,599
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/127,598
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/130,412
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/130,696
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 60/131,278
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131,673
;  PRIOR FILING DATE: 1999-04-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-382-837-3

  Query Match             95.7%;  Score 779;  DB 7;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 5.8e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 7
US-11-377-165A-3
; Sequence 3, Application US/11377165A
; Publication No. US20060198784A1
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
```

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;  TITLE OF INVENTION: Methods of Treatment Using Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C7
;  CURRENT APPLICATION NUMBER: US/11/377,165A
;  CURRENT FILING DATE:  2006-03-17
;  PRIOR APPLICATION NUMBER: 09/589,288
;  PRIOR FILING DATE: 2000-06-08
;  PRIOR APPLICATION NUMBER: 09/507,968
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/122,388
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: 60/124,097
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/126,599
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/127,598
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/130,412
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/130,696
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 60/131,278
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131,673
;  PRIOR FILING DATE: 1999-04-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-377-165A-3

  Query Match            95.7%;  Score 779;  DB 7;  Length 233;
  Best Local Similarity  96.2%;  Pred. No. 5.8e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 8
US-11-337-690-5
; Sequence 5, Application US/11337690
; Publication No. US20060171918A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruben, Steven M
;        TITLE OF INVENTION: Apoptosis Inducing Molecule I
;        NUMBER OF SEQUENCES: 10
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: US
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/337,690
;             FILING DATE: 24-Jan-2006
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/816,981
;             FILING DATE: 13-MAR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kimball, Paul, C.
;             REGISTRATION NUMBER: 34,610
;             REFERENCE/DOCKET NUMBER: PF261
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (301) 309-8504
;             TELEFAX: (301) 309-8512
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 233 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-337-690-5

  Query Match            94.6%;  Score 770;  DB 7;  Length 233;
  Best Local Similarity  95.5%;  Pred. No. 5.4e-75;
  Matches  150;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              | ||||| |||||||||||||||||||||||||||||
Db        197 GCVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 9
US-11-315-825-28
; Sequence 28, Application US/11315825
; Publication No. US20060141573A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/11/315,825
;  CURRENT FILING DATE:  2005-12-22
;  PRIOR APPLICATION NUMBER: US/09/247,225
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 28
;   LENGTH: 150
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-315-825-28

  Query Match            91.9%;  Score 748;  DB 7;  Length 150;
  Best Local Similarity  96.0%;  Pred. No. 7.1e-73;
  Matches  144;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 PSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFSGQ 67
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ 60
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Qy         68 GCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
              ||||||||||||||||||||||| |||||||:|||||||||||||| ||||||||||||||
Db         61 GCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLE 120

Qy        128 PGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||||||||||||||||||||||||||
Db        121 KGDRLSAEINRPDYLDFAESGQVYFGIIAL 150


RESULT 10
US-10-794-755-5
; Sequence 5, Application US/10794755
; Publication No. US20060136136A1
; GENERAL INFORMATION:
;  APPLICANT: KARPUSAS, MICHAEL
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF BAFF, AND USE THEREOF IN DRUG
;  TITLE OF INVENTION:  DESIGN
;  FILE REFERENCE: A135CON1
;  CURRENT APPLICATION NUMBER: US/10/794,755
;  CURRENT FILING DATE:  2004-03-05
;  PRIOR APPLICATION NUMBER: PCT/US02/28579
;  PRIOR FILING DATE: 2002-09-06
;  PRIOR APPLICATION NUMBER: 60/317,524
;  PRIOR FILING DATE: 2001-09-06
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
;   LENGTH: 152
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Illustrative
;   OTHER INFORMATION: peptide TNFa
US-10-794-755-5

  Query Match             91.9%;  Score 748;  DB 6;  Length 152;
  Best Local Similarity   95.4%;  Pred. No. 7.2e-73;
  Matches  145;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          6 RTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFS 65
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFK 60

Qy         66 GQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQ 125
              ||||||||||||||||||||||| |||||||:|||||||||||||| ||||||||||||
Db         61 GQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQ 120

Qy        126 LEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              || |||||||||||||| ||||||||||||||
Db        121 LEKGDRLSAEINRPDYLLFAESGQVYFGIIAL 152


RESULT 11
US-10-527-832-6
; Sequence 6, Application US/10527832
; Publication No. US20060149034A1
; GENERAL INFORMATION:
;  APPLICANT: Cornell Research Foundation
;  TITLE OF INVENTION: Homing Peptides to Receptors of Heart Vasculature
;  FILE REFERENCE: 955-39 PCT US
;  CURRENT APPLICATION NUMBER: US/10/527,832
;  CURRENT FILING DATE:  2005-03-15
;  PRIOR APPLICATION NUMBER: US 60/412,330
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: PCT/US03/29379
;  PRIOR FILING DATE: 2003-09-18
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 152
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-527-832-6

  Query Match             91.9%;  Score 748;  DB 6;  Length 152;
  Best Local Similarity   95.4%;  Pred. No. 7.2e-73;
  Matches  145;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          6 RTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFS 65
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFK 60

Qy         66 GQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQ 125
              ||||||||||||||||||||||| |||||||:|||||||||||||| ||||||||||||
Db         61 GQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQ 120

Qy        126 LEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              || |||||||||||||| ||||||||||||||
Db        121 LEKGDRLSAEINRPDYLLFAESGQVYFGIIAL 152


RESULT 12
US-11-241-106-8
; Sequence 8, Application US/11241106
; Publication No. US20060159654A1
;  GENERAL INFORMATION:
;    APPLICANT:  Choi, Yongwon
;    APPLICANT:  Wong, Brian
;    APPLICANT:  Josien, Regis
;    APPLICANT:  Steinman, Ralph
;    TITLE OF INVENTION:  A PROTEIN BELONGING TO THE TNF  SUPERFAMILY
;    TITLE OF INVENTION:  INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS
;    TITLE OF INVENTION:  ENCODING SAME, AND
;    TITLE OF INVENTION:  METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/241,106
;      FILING DATE:  30-Sept-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  A) APPLICATION NUMBER: US/09/873,829
;      FILING DATE:  04-Jun-2001
;      APPLICATION NUMBER:  09/210,115
;      FILING DATE:  <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-200 CIP N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  235 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mus musculus
US-11-241-106-8
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  Query Match           77.9%;  Score 634.5;  DB 7;  Length 235;
  Best Local Similarity  75.2%;  Pred. No. 1.9e-60;
  Matches  118;  Conservative   21;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| | | ||:||::||||||||::|:|||||||::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYS 139

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||  :||||||:|| |:||  ||||||::||| ::|||||| ||||||||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYL 198

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||:||||:| | ||||||||||||:|||
Db        199 GGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 13
US-10-794-755-6
; Sequence 6, Application US/10794755
; Publication No. US20060136136A1
; GENERAL INFORMATION:
;  APPLICANT: KARPUSAS, MICHAEL
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF BAFF, AND USE THEREOF IN DRUG
;  TITLE OF INVENTION:  DESIGN
;  FILE REFERENCE: A135CON1
;  CURRENT APPLICATION NUMBER: US/10/794,755
;  CURRENT FILING DATE:  2004-03-05
;  PRIOR APPLICATION NUMBER: PCT/US02/28579
;  PRIOR FILING DATE: 2002-09-06
;  PRIOR APPLICATION NUMBER: 60/317,524
;  PRIOR FILING DATE: 2001-09-06
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
;   LENGTH: 147
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Illustrative
;   OTHER INFORMATION: peptide LTa
US-10-794-755-6

  Query Match           26.2%;  Score 213.5;  DB 6;  Length 147;
  Best Local Similarity  34.0%;  Pred. No. 1.7e-15;
  Matches   51;  Conservative   25;  Mismatches   63;  Indels   11;  Gaps    4;

Qy         12 PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFSGQG--- 68
              | ||:: :|  :  | |      | | :|  | :| |:||: |:| :||||:|||:
Db          4 PAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSP 63

Qy         69 -CPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
               |: : | | :   :  |   | |||:     |:    | :  ||   :| |  |||
Db         64 KATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQLT 117

Qy        128 PGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||:||   :   :|  : |  |:||  ||
Db        118 QGDQLSTHTDGIPHLVLSPS-TVFFGAFAL 146


RESULT 14
US-11-315-825-31
; Sequence 31, Application US/11315825
; Publication No. US20060141573A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/11/315,825
;  CURRENT FILING DATE:  2005-12-22
;  PRIOR APPLICATION NUMBER: US/09/247,225
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 31
;   LENGTH: 147
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-315-825-31

  Query Match           26.2%;  Score 213.5;  DB 7;  Length 147;
  Best Local Similarity  34.0%;  Pred. No. 1.7e-15;
  Matches   51;  Conservative   25;  Mismatches   63;  Indels   11;  Gaps    4;

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Db          5 PAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSP 64

Qy         69 -CPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
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Db         65 KATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQLT 118

Qy        128 PGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 15
US-11-382-837-4
; Sequence 4, Application US/11382837
; Publication No. US20060193859A1
; GENERAL INFORMATION:
;  APPLICANT: Yu et al.
;  TITLE OF INVENTION: Methods of Treatment Using Antibodies to Neutrokine-alpha
;  FILE REFERENCE: PF343P3C8
;  CURRENT APPLICATION NUMBER: US/11/382,837
;  CURRENT FILING DATE:  2006-05-11
;  PRIOR APPLICATION NUMBER: 09/589,288
;  PRIOR FILING DATE: 2000-06-08
;  PRIOR APPLICATION NUMBER: 09/507,968
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: 60/122,388
;  PRIOR FILING DATE: 1999-03-02
;  PRIOR APPLICATION NUMBER: 60/124,097
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/126,599
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/127,598
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: 60/130,412
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 60/130,696
;  PRIOR FILING DATE: 1999-04-23
;  PRIOR APPLICATION NUMBER: 60/131,278
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131,673
;  PRIOR FILING DATE: 1999-04-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-382-837-4

  Query Match           26.2%;  Score 213.5;  DB 7;  Length 205;
  Best Local Similarity  34.0%;  Pred. No. 2.6e-15;
  Matches   51;  Conservative   25;  Mismatches   63;  Indels   11;  Gaps    4;
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Qy          12 PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFSGQG--- 68
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Db          63 PAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSP 122

Qy          69 -CPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYLGGVFQLE 127
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Qy         128 PGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Search completed: September 16, 2006, 09:55:42
Job time : 35 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 16, 2006, 09:51:17 ; Search time 179 Seconds
(without alignments)
406.283 Million cell updates/sec

Title: US-10-668-178-3
Perfect score: 814
Sequence: 1 VRSSSRTPSDMPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	814	100.0	157	4	US-10-354-985-3	Sequence 3, Appli
2	814	100.0	157	5	US-10-668-178-3	Sequence 3, Appli
3	814	100.0	157	5	US-10-668-178-13	Sequence 13, Appl
4	779	95.7	157	3	US-09-756-301A-1	Sequence 1, Appli
5	779	95.7	157	3	US-09-927-703-1	Sequence 1, Appli
6	779	95.7	157	3	US-09-854-280-19	Sequence 19, Appl
7	779	95.7	157	3	US-09-934-465-13	Sequence 13, Appl
8	779	95.7	157	3	US-09-766-535A-1	Sequence 1, Appli
9	779	95.7	157	3	US-09-854-208-19	Sequence 19, Appl
10	779	95.7	157	3	US-09-756-161A-1	Sequence 1, Appli
11	779	95.7	157	3	US-09-903-327A-7	Sequence 7, Appli
12	779	95.7	157	3	US-09-756-398B-1	Sequence 1, Appli
13	779	95.7	157	3	US-09-897-724-1	Sequence 1, Appli
14	779	95.7	157	4	US-10-010-229-1	Sequence 1, Appli
15	779	95.7	157	4	US-10-043-450-1	Sequence 1, Appli
16	779	95.7	157	4	US-10-044-534-1	Sequence 1, Appli
17	779	95.7	157	4	US-10-099-007A-1	Sequence 1, Appli
18	779	95.7	157	4	US-10-043-432-1	Sequence 1, Appli
19	779	95.7	157	4	US-10-119-621-1	Sequence 1, Appli
20	779	95.7	157	4	US-10-208-145-1	Sequence 1, Appli
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22	779	95.7	157	4	US-10-305-347A-9	Sequence 9, Appli
23	779	95.7	157	4	US-10-198-845-1	Sequence 1, Appli
24	779	95.7	157	4	US-10-227-488-1	Sequence 1, Appli
25	779	95.7	157	4	US-10-170-812-7	Sequence 7, Appli
26	779	95.7	157	4	US-10-187-121-1	Sequence 1, Appli
27	779	95.7	157	4	US-10-176-460-1	Sequence 1, Appli
28	779	95.7	157	4	US-10-186-559-1	Sequence 1, Appli
29	779	95.7	157	4	US-10-371-961-1	Sequence 1, Appli
30	779	95.7	157	4	US-10-200-795-1	Sequence 1, Appli
31	779	95.7	157	4	US-10-319-011-1	Sequence 1, Appli
32	779	95.7	157	4	US-10-371-443-1	Sequence 1, Appli
33	779	95.7	157	4	US-10-379-866-1	Sequence 1, Appli
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35	779	95.7	157	4	US-10-354-985-1	Sequence 1, Appli
36	779	95.7	157	4	US-10-397-786A-1	Sequence 1, Appli
37	779	95.7	157	4	US-10-665-971-1	Sequence 1, Appli
38	779	95.7	157	4	US-10-637-759-1	Sequence 1, Appli
39	779	95.7	157	4	US-10-327-619-1	Sequence 1, Appli
40	779	95.7	157	4	US-10-774-118-1	Sequence 1, Appli
41	779	95.7	157	4	US-10-394-471B-17	Sequence 17, Appl
42	779	95.7	157	5	US-10-861-685-13	Sequence 13, Appl
43	779	95.7	157	5	US-10-668-178-1	Sequence 1, Appli
44	779	95.7	157	5	US-10-957-134-1	Sequence 1, Appli
45	779	95.7	157	5	US-10-727-155-265	Sequence 265, App

ALIGNMENTS

RESULT 1
US-10-354-985-3
; Sequence 3, Application US/10354985
; Publication No. US20040001802A1
; GENERAL INFORMATION:
; APPLICANT: MAYUMI, Tandanori et al.
; TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE COMPLEX
; FILE REFERENCE: MAYUMI=2
; CURRENT APPLICATION NUMBER: US/10/354,985
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: JP 083509/2002
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: JP 1185387/2002
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Variant protein of human tumor necrosis factor
US-10-354-985-3

Query Match 100.0%; Score 814; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 2
US-10-668-178-3
; Sequence 3, Application US/10668178
; Publication No. US20050013795A1
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
; APPLICANT: MAYUMI, Tadanori
; APPLICANT: TSUTSUMI, Yasuo
; APPLICANT: NAKAGAWA, Shinsaku

```
;  APPLICANT:  IKEGAMI, Hakuo
;  TITLE OF INVENTION: Biologically-active conjugate
;  FILE REFERENCE: MAYUMI2A
;  CURRENT APPLICATION NUMBER: US/10/668,178
;  CURRENT FILING DATE:  2003-09-24
;  PRIOR APPLICATION NUMBER: JP 83509/2002
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: JP 185387/2002
;  PRIOR FILING DATE: 2002-06-26
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic (Variant protein of human tumor necrosis factor)
US-10-668-178-3

  Query Match           100.0%;  Score 814;  DB 5;  Length 157;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-80;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 3
US-10-668-178-13
; Sequence 13, Application US/10668178
; Publication No. US20050013795A1
; GENERAL INFORMATION:
;  APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
;  APPLICANT:  MAYUMI, Tadanori
;  APPLICANT:  TSUTSUMI, Yasuo
;  APPLICANT:  NAKAGAWA, Shinsaku
;  APPLICANT:  IKEGAMI, Hakuo
;  TITLE OF INVENTION: Biologically-active conjugate
;  FILE REFERENCE: MAYUMI2A
;  CURRENT APPLICATION NUMBER: US/10/668,178
;  CURRENT FILING DATE:  2003-09-24
;  PRIOR APPLICATION NUMBER: JP 83509/2002
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: JP 185387/2002
;  PRIOR FILING DATE: 2002-06-26
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-668-178-13

  Query Match           100.0%;  Score 814;  DB 5;  Length 157;
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Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 4
US-09-756-301A-1
; Sequence 1, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-008
;  CURRENT APPLICATION NUMBER: US/09/756,301A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S.07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-756-301A-1

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  Best Local Similarity  96.2%;  Pred. No. 1.9e-76;
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RESULT 5
US-09-927-703-1
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; Sequence 1, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/09/927,703
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-927-703-1

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

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Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 6
US-09-854-280-19
; Sequence 19, Application US/09854280
; Patent No. US20020052027A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Li, Hanzhong
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C2
;  CURRENT APPLICATION NUMBER: US/09/854,280
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/085,579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 60/113,621
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

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              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 7
US-09-934-465-13
; Sequence 13, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  TITLE OF INVENTION: APO-2 LIGAND
;  FILE REFERENCE: 11669.22US03
;  CURRENT APPLICATION NUMBER: US/09/934,465
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 08/584,031
;  PRIOR FILING DATE: 1996-01-09
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-934-465-13

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 8
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US-09-766-535A-1
; Sequence 1, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-010
;  CURRENT APPLICATION NUMBER: US/09/766,535A
;  CURRENT FILING DATE:  2001-01-18
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-766-535A-1

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 9
US-09-854-208-19
; Sequence 19, Application US/09854208
; Patent No. US20020106743A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Li, Hanzhong
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: P1381-R1
;  CURRENT APPLICATION NUMBER: US/09/854,208
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: US/09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/085,579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 60/113,621
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-854-208-19

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 10
US-09-756-161A-1
; Sequence 1, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-007
;  CURRENT APPLICATION NUMBER: US/09/756,161A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S.07/670,827
;  PRIOR FILING DATE: 1991-03-18
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;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;    LENGTH: 157
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-756-161A-1

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 11
US-09-903-327A-7
; Sequence 7, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
;  APPLICANT: Nemerow, Glen R.
;  APPLICANT:  Li, Erguang
;  TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
;  TITLE OF INVENTION:  GENE
;  TITLE OF INVENTION:  DELIVERY
;  FILE REFERENCE: 22908-1228
;  CURRENT APPLICATION NUMBER: US/09/903,327A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 09/613,017
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;    LENGTH: 157
;    TYPE: PRT
;    ORGANISM: Human
;    FEATURE:
;    NAME/KEY: PEPTIDE
;    LOCATION: (0)...(0)
;    OTHER INFORMATION: Tumor necrosis factor-alpha (TNF alpha, mature
;    OTHER INFORMATION: peptide)
US-09-903-327A-7

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 12
US-09-756-398B-1
; Sequence 1, Application US/09756398B
; Publication No. US20030017584A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-006
;  CURRENT APPLICATION NUMBER: US/09/756,398B
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S.07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;    LENGTH: 157
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-756-398B-1

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 13
US-09-897-724-1
; Sequence 1, Application US/09897724
; Publication No. US20030175837A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
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;  FILE REFERENCE: 0975.1005-012
;  CURRENT APPLICATION NUMBER: US/09/897,724
;  CURRENT FILING DATE:  2001-07-02
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S.07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-897-724-1

  Query Match             95.7%;  Score 779;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 14
US-10-010-229-1
; Sequence 1, Application US/10010229
; Publication No. US20020114805A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/10/010,229
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US/09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-010-229-1

  Query Match             95.7%;  Score 779;  DB 4;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 15
US-10-043-450-1
; Sequence 1, Application US/10043450
; Publication No. US20020141996A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/10/043,450
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-043-450-1

  Query Match             95.7%;  Score 779;  DB 4;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-76;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Search completed: September 16, 2006, 09:55:03
Job time : 180 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 16, 2006, 09:50:32 ; Search time 50 Seconds
(without alignments)
274.846 Million cell updates/sec

Title: US-10-668-178-3
Perfect score: 814
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	779	95.7	157	1	US-07-794-400-1	Sequence 1, Appli
2	779	95.7	157	1	US-08-041-648-2	Sequence 2, Appli
3	779	95.7	157	1	US-08-107-235-1	Sequence 1, Appli
4	779	95.7	157	1	US-08-217-529-2	Sequence 2, Appli
5	779	95.7	157	1	US-08-318-193-86	Sequence 86, Appl
6	779	95.7	157	1	US-08-397-470-1	Sequence 1, Appli
7	779	95.7	157	1	US-08-192-102-1	Sequence 1, Appli
8	779	95.7	157	1	US-08-324-799-1	Sequence 1, Appli
9	779	95.7	157	1	US-08-538-875-1	Sequence 1, Appli
10	779	95.7	157	1	US-08-394-600B-17	Sequence 17, Appl
11	779	95.7	157	1	US-08-500-860A-35	Sequence 35, Appl
12	779	95.7	157	1	US-08-192-861A-1	Sequence 1, Appli
13	779	95.7	157	1	US-08-600-783-5	Sequence 5, Appli
14	779	95.7	157	2	US-08-584-031-13	Sequence 13, Appl
15	779	95.7	157	2	US-08-714-960B-1	Sequence 1, Appli
16	779	95.7	157	2	US-09-133-119-1	Sequence 1, Appli
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18	779	95.7	157	2	US-09-598-784-1	Sequence 1, Appli
19	779	95.7	157	2	US-09-496-118B-7	Sequence 7, Appli
20	779	95.7	157	2	US-08-395-456C-17	Sequence 17, Appl
21	779	95.7	157	2	US-08-487-453A-17	Sequence 17, Appl
22	779	95.7	157	2	US-09-582-450-13	Sequence 13, Appl
23	779	95.7	157	2	US-09-934-465-13	Sequence 13, Appl
24	779	95.7	157	2	US-09-756-301B-1	Sequence 1, Appli
25	779	95.7	157	2	US-09-756-398B-1	Sequence 1, Appli
26	779	95.7	157	2	US-09-766-535A-1	Sequence 1, Appli
27	779	95.7	157	2	US-09-459-808-13	Sequence 13, Appl
28	779	95.7	157	5	PCT-US92-02190-1	Sequence 1, Appli
29	779	95.7	157	5	PCT-US93-02475-1	Sequence 1, Appli
30	779	95.7	157	5	PCT-US95-02513-17	Sequence 17, Appl
31	779	95.7	157	7	5180811-1	Patent No. 5180811
32	779	95.7	158	2	US-09-645-415A-4	Sequence 4, Appli
33	779	95.7	177	1	US-08-394-600B-21	Sequence 21, Appl
34	779	95.7	177	2	US-08-395-456C-21	Sequence 21, Appl
35	779	95.7	177	2	US-08-487-453A-21	Sequence 21, Appl
36	779	95.7	177	5	PCT-US95-02513-21	Sequence 21, Appl
37	779	95.7	180	2	US-09-645-415A-8	Sequence 8, Appli
38	779	95.7	193	1	US-08-889-909A-3	Sequence 3, Appli
39	779	95.7	193	2	US-09-156-163A-3	Sequence 3, Appli
40	779	95.7	193	2	US-09-982-308B-3	Sequence 3, Appli
41	779	95.7	233	1	US-08-323-445A-10	Sequence 10, Appl
42	779	95.7	233	1	US-08-515-903A-10	Sequence 10, Appl
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44	779	95.7	233	1	US-08-230-428B-2	Sequence 2, Appli
45	779	95.7	233	2	US-08-883-086-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-07-794-400-1
; Sequence 1, Application US/07794400
; Patent No. 5422104
; GENERAL INFORMATION:
;   APPLICANT: Fiers, W.
;   APPLICANT: Tavernier, J.
;   APPLICANT: Van Ostade, X.
;   TITLE OF INVENTION: TNF-Muteins
;   NUMBER OF SEQUENCES: 24
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Hoffmann-La Roche Inc.
;     STREET: 340 Kingsland Street
;     CITY: Nutley
;     STATE: New Jersey
;     COUNTRY: USA
;     ZIP: 07110
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/794,400
;     FILING DATE: 19911120
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 90810901.0
;     FILING DATE: 21-NOV-1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Krovatin, William
;     REGISTRATION NUMBER: 33256
;     REFERENCE/DOCKET NUMBER: 4105/136-00
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (201) 235-4387
;     TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 157 amino acids
;     TYPE: AMINO ACID
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;     ORGANISM: Homo sapiens
;     TISSUE TYPE: Blood
;     CELL TYPE: Macrophage
US-07-794-400-1

  Query Match 95.7%; Score 779; DB 1; Length 157;
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  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 2
US-08-041-648-2
; Sequence 2, Application US/08041648
; Patent No. 5486463
;  GENERAL INFORMATION:
;    APPLICANT:  Lesslauer, Werner
;    APPLICANT:  L tscher, Hansruedi
;    APPLICANT:  St ber, Dietrich
;    TITLE OF INVENTION:  TNF-MUTEINS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/041,648
;      FILING DATE:  1-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 92810249.0
;      FILING DATE:  2-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Roseman, Catherine R.
;      REGISTRATION NUMBER:  34240
;      REFERENCE/DOCKET NUMBER:  RAN 4105/147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6208
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-041-648-2

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
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  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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RESULT 3
US-08-107-235-1
; Sequence 1, Application US/08107235
; Patent No. 5587457
;  GENERAL INFORMATION:
;    APPLICANT:  Rathjen, Deborah A
;    APPLICANT:  Ferrante, Antonio
;    APPLICANT:  Widmer, Fred
;    TITLE OF INVENTION:  Neutrophil Stimulating Peptides
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 S. Wacker Dr.
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/107,235
;      FILING DATE:  16-AUG-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/930,415
;      FILING DATE:  12-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDonnell, John J
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,622A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..157
;      OTHER INFORMATION:  /note= "HUMAN TNF)"
US-08-107-235-1

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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RESULT 4
US-08-217-529-2
; Sequence 2, Application US/08217529
; Patent No. 5597899
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;  GENERAL INFORMATION:
;    APPLICANT:  Banner, David
;    APPLICANT:  Lesslauer, Werner
;    APPLICANT:  Lotscher, Hansreudi
;    APPLICANT:  Stuber, Dietrich
;    TITLE OF INVENTION:  Tumor Necrosis Factor Muteins
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,529
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93810224.1
;      FILING DATE:  29-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Roseman, Catherine R
;      REGISTRATION NUMBER:  34240
;      REFERENCE/DOCKET NUMBER:  4105/155
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6208
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-217-529-2

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 5
US-08-318-193-86
; Sequence 86, Application US/08318193
; Patent No. 5641663
;  GENERAL INFORMATION:
;    APPLICANT:  GARVIN, Robert T.
;    APPLICANT:  MALEK, Lawrence T.
;    TITLE OF INVENTION:  AN EXPRESSION SYSTEM FOR THE SECRETION
;    TITLE OF INVENTION:  OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
;    TITLE OF INVENTION:  STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
;    TITLE OF INVENTION:  PROTEINS FROM STREPTOMYCES
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,193
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,314
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/224,568
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  18740/116 CACO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  86:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-193-86

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 6
US-08-397-470-1
; Sequence 1, Application US/08397470
; Patent No. 5652353
;  GENERAL INFORMATION:
;    APPLICANT:  Fiers, W.
;    APPLICANT:  Tavernier, J.
;    APPLICANT:  Van Ostade, X.
;    TITLE OF INVENTION:  TNF-Muteins
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/397,470
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/794,400
;      FILING DATE:  20-NOV-1991
;      APPLICATION NUMBER:  EP 90810901.0
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Krovatin, William
;      REGISTRATION NUMBER:  33256
;      REFERENCE/DOCKET NUMBER:  4105/136-00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4387
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  Blood
;      CELL TYPE:  Macrophage
US-08-397-470-1

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
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Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 7
US-08-192-102-1
; Sequence 1, Application US/08192102
; Patent No. 5656272
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,102
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,093
;      FILING DATE:  04-FEB-1994
;      APPLICATION NUMBER:  US 08/013,413
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/010,406
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,852
;      FILING DATE:  11-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,606
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/670,827
;      FILING DATE:  18-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  NYU93-01M3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-192-102-1

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 8
US-08-324-799-1
; Sequence 1, Application US/08324799
; Patent No. 5698195
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES AND PEPTIDES
;    TITLE OF INVENTION:  OF HUMAN TUMOR NECROSIS FACTOR
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/324,799
;       FILING DATE:  18-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/192,093
;       FILING DATE:  04-FEB-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/192,102
;       FILING DATE:  04-FEB-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/192,861
;       FILING DATE:  04-FEB-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/013,413
;       FILING DATE:  02-FEB-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/010,406
;       FILING DATE:  29-JAN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/943,852
;       FILING DATE:  11-SEP-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/853,606
;       FILING DATE:  18-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/670,827
;       FILING DATE:  18-MAR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brook, David E.
;       REGISTRATION NUMBER:  22,592
;       REFERENCE/DOCKET NUMBER:  NYU93-01M4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 861-6240
;       TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  157 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-324-799-1

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 9
US-08-538-875-1
; Sequence 1, Application US/08538875
; Patent No. 5773582
;  GENERAL INFORMATION:
;     APPLICANT:  Shin, Hang-Cheol
;     APPLICANT:  Shin, Nam-Kyu
;     APPLICANT:  Lee, Inkyung
;     APPLICANT:  Kang, Sungzong
;     TITLE OF INVENTION:  TUMOR NECROSIS FACTOR MUTEINS
;     NUMBER OF SEQUENCES:  73
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Shin, Hang-Cheol
;       STREET:  Jukong Gocheung Apt. 1014-806, Haan-dong
;       CITY:  Kwangmyung-shi
;       STATE:  Kyungki-do
;       COUNTRY:  Republic of Korea
;       ZIP:  423-060
;       ADDRESSEE:  Shin, Nam-Kyu
;       STREET:  #181-404 Sadang-4-dong, Dongjak-ku
;       CITY:  Seoul
;       STATE:
;       COUNTRY:  Republic of Korea
;       ZIP:  156-094
;       ADDRESSEE:  Lee, Inkyung
;       STREET:  11/2, #302-39 Juan-4-dong, Nam-ku
;       CITY:  Incheon
;       STATE:
;       COUNTRY:  Republic of Korea
;       ZIP:  402-204
;       ADDRESSEE:  Kang, Sungzong
;       STREET:  #84-4 Daeshin-dong, Seodaemun-ku
;       CITY:  Seoul
;       STATE:
;       COUNTRY:  Republic of Korea
;       ZIP:  120-160
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette 3.5inch 2.0Mb storage
;       COMPUTER:  IBM PC/AT
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/538,875
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/193,336
;       FILING DATE:
;       APPLICATION NUMBER:  KR 93-1751
;       FILING DATE:  9-FEB-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:
;       REGISTRATION NUMBER:
;       REFERENCE/DOCKET NUMBER:
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:
;       TELEFAX:
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  157 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-538-875-1

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 10
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US-08-394-600B-17
; Sequence 17, Application US/08394600B
; Patent No. 5843693
;  GENERAL INFORMATION:
;    APPLICANT:  Halenbeck, Robert F.
;    APPLICANT:  Jewell, David A.
;    APPLICANT:  Koths, Kirston E.
;    APPLICANT:  Kriegler, Michael
;    APPLICANT:  Perez, Carl
;    TITLE OF INVENTION:  Compositions for the Inhibition of
;    TITLE OF INVENTION:  Protein Hormone Formation and Uses Thereof
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street; 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/394,600B
;      FILING DATE:  02/27/95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Donald J. Pochopien
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  820.005/11850US05
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-394-600B-17

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 11
US-08-500-860A-35
; Sequence 35, Application US/08500860A
; Patent No. 5891679
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, RUDOLPH
;    APPLICANT:  DE BAETSELIER, PATRICK
;    APPLICANT:  FRANSEN, LUCIE
;    APPLICANT:  SABLON, ERWIN
;    TITLE OF INVENTION:  TNF-MUTEINS, A PROCESS FOR PREPARING THEM AND
;    TITLE OF INVENTION:  THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,860A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BYRNE, THOMAS E.
;      REGISTRATION NUMBER:  32,205
;      REFERENCE/DOCKET NUMBER:  1487-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4000
;      TELEFAX:  (703)816-4100
;      TELEX:  200797 NIXN UR
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-500-860A-35

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 12
US-08-192-861A-1
; Sequence 1, Application US/08192861A
; Patent No. 5919452
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  METHODS OF TREATING TNF`-MEDIATED DISEASE USING
;    TITLE OF INVENTION:  CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/192,861A
;       FILING DATE:  04-FEB-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/013,413
;       FILING DATE:  02-FEB-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/010,406
;       FILING DATE:  29-JAN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/943,852
;       FILING DATE:  11-SEP-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/853,606
;       FILING DATE:  18-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/670,827
;       FILING DATE:  18-MAR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brook, David E.
;       REGISTRATION NUMBER:  22,592
;       REFERENCE/DOCKET NUMBER:  NYU93-01M2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (781) 861-6240
;       TELEFAX:  (781) 861-9540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  157 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-192-861A-1

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:|||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 13
US-08-600-783-5
; Sequence 5, Application US/08600783
; Patent No. 5962267
;  GENERAL INFORMATION:
;    APPLICANT:  SHIN, Hang Cheol
;    APPLICANT:  CHANG, Seung Gu
;    APPLICANT:  KIM, Dae Young
;    APPLICANT:  KIM, Chong Suhl
;    TITLE OF INVENTION:  Proinsulin Derivative and Process
;    TITLE OF INVENTION:  for Producing Human Insulin
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SHIN, Hang Cheol
;      STREET:  Ssangma-Hanshin Apt. 102-1206,
;      STREET:  #245 Cholsan-dong
;      CITY:  Kwangmyung-shi
;      STATE:  Kyungki-do
;      COUNTRY:  Republic of Korea
;      ZIP:  423-030
;      ADDRESSEE:  CHANG, Seung Gu
;      STREET:  Hyundai Apt. 71-203, Apkujong-dong,
;      STREET:  Kangnam-ku
;      CITY:  Seoul
;      STATE:  Seoul
;      COUNTRY:  Republic of Korea
;      ZIP:  135-110
;      ADDRESSEE:  KIM, Dae Young
;      STREET:  Sosa Jukong Apt. 108-202, Sosa Bon-dong,
;      STREET:  Sosa-ku
;      CITY:  Bucheon-shi
;      STATE:  Kyungki-do
;      COUNTRY:  Republic of Korea
;      ZIP:  422-230
;      ADDRESSEE:  KIM, Chong Suhl
;      STREET:  Garden Heights Apt. 202-801, #100,
;      STREET:  Hwangkeum-dong, Soosung-ku
;      CITY:  Taegu
;      STATE:  Taegu
;      COUNTRY:  Republic of Korea
;      ZIP:  706-040
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk, 3.5 inch, 1.44MB storage
;      COMPUTER:  IBM PC/AT
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/600,783
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  KR 95-2751
;      FILING DATE:  15-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Shahan Islam
;      REGISTRATION NUMBER:  32,507
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-1000
;      TELEFAX:  (212) 953-7249
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-600-783-5

  Query Match             95.7%;  Score 779;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:|||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 14
US-08-584-031-13
; Sequence 13, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  TITLE OF INVENTION: APO-2 LIGAND
```

```
;  FILE REFERENCE: 11669.22US03
;  CURRENT APPLICATION NUMBER: US/08/584,031A
;  CURRENT FILING DATE: 1996-01-09
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-584-031-13

  Query Match             95.7%;  Score 779;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:|||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 15
US-08-714-960B-1
; Sequence 1, Application US/08714960B
; Patent No. 6121237
;  GENERAL INFORMATION:
;    APPLICANT:  RATHJEN, Deborah A
;    APPLICANT:  FERRANTE, Antonio
;    TITLE OF INVENTION:  Neutrophil Stimulating Peptides
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF, LTD.
;      STREET:  10 S. Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 Mb storage diskette, 3.50 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  IBM compatible PC/MS-DOS
;      SOFTWARE:  WordPerfect version 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,960B
;      FILING DATE:  17-SEP-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PJ9065
;      FILING DATE:  12-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU91/00086
;      FILING DATE:  12-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/930,415
;      FILING DATE:  09-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/107,235
;      FILING DATE:  16-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resis, Robert H.
;      REGISTRATION NUMBER:  32,168
;      REFERENCE/DOCKET NUMBER:  92,622-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..157
;      OTHER INFORMATION:  /note= "Human TNF"
US-08-714-960B-1

  Query Match             95.7%;  Score 779;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1e-73;
  Matches  151;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||| |||||||||||||||||||||| |||||||:|||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


Search completed: September 16, 2006, 09:51:57
Job time : 51 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 16, 2006, 09:40:57 ; Search time 195 Seconds
(without alignments)
368.118 Million cell updates/sec

Title: US-10-668-178-3
Perfect score: 814
Sequence: 1 VRSSSRTPSDMPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	814	100.0	157	8	ADH10160	Adh10160 Human tum
2	807	99.1	157	9	AEB45433	Aeb45433 TNF-R1 sp
3	806	99.0	157	9	AEB45432	Aeb45432 TNF-R1 sp
4	805	98.9	157	9	AEB45434	Aeb45434 TNF-R1 sp
5	803	98.6	157	9	AEB45430	Aeb45430 TNF-R1 sp
6	800	98.3	157	9	AEB45453	Aeb45453 TNF-R2 sp
7	799	98.2	157	9	AEB45431	Aeb45431 TNF-R1 sp
8	795	97.7	157	9	AEB45454	Aeb45454 TNF-R2 sp
9	793	97.4	157	9	AEB45469	Aeb45469 TNF-R2 sp
10	792	97.3	157	9	AEB45438	Aeb45438 TNF-R1 sp
11	792	97.3	157	9	AEB45436	Aeb45436 TNF-R1 sp
12	792	97.3	157	9	AEB45461	Aeb45461 TNF-R2 sp
13	791	97.2	157	9	AEB45460	Aeb45460 TNF-R2 sp
14	791	97.2	157	9	AEB45464	Aeb45464 TNF-R2 sp
15	790	97.1	157	9	AEB45472	Aeb45472 TNF-R2 sp
16	790	97.1	157	9	AEB45471	Aeb45471 TNF-R2 sp
17	790	97.1	157	9	AEB45455	Aeb45455 TNF-R2 sp
18	790	97.1	157	9	AEB45466	Aeb45466 TNF-R2 sp
19	790	97.1	157	9	AEB45474	Aeb45474 TNF-R2 sp
20	790	97.1	157	9	AEB45457	Aeb45457 TNF-R2 sp
21	790	97.1	157	9	AEB45475	Aeb45475 TNF-R2 sp
22	789	96.9	157	9	AEB45458	Aeb45458 TNF-R2 sp
23	789	96.9	157	9	AEB45473	Aeb45473 TNF-R2 sp
24	789	96.9	157	9	AEB45467	Aeb45467 TNF-R2 sp
25	789	96.9	157	9	AEB45468	Aeb45468 TNF-R2 sp
26	788	96.8	157	9	AEB45437	Aeb45437 TNF-R1 sp
27	788	96.8	157	9	AEB45462	Aeb45462 TNF-R2 sp
28	788	96.8	157	9	AEB45470	Aeb45470 TNF-R2 sp
29	787	96.7	157	9	AEB45456	Aeb45456 TNF-R2 sp
30	787	96.7	157	9	AEB45459	Aeb45459 TNF-R2 sp
31	787	96.7	157	9	AEB45465	Aeb45465 TNF-R2 sp
32	787	96.7	157	9	AEB45463	Aeb45463 TNF-R2 sp
33	785	96.4	157	9	AEB45429	Aeb45429 TNF-R1 sp
34	784	96.3	157	9	AEB45428	Aeb45428 TNF-R1 sp
35	784	96.3	157	9	AEB45425	Aeb45425 TNF-R1 sp
36	783	96.2	157	9	AEB45421	Aeb45421 Human TNF
37	782	96.1	157	9	AEB45427	Aeb45427 TNF-R1 sp
38	782	96.1	157	9	AEB45423	Aeb45423 Human TNF
39	782	96.1	157	9	AEB45435	Aeb45435 TNF-R1 sp
40	780	95.8	157	2	AAR62465	Aar62465 Tumour ne
41	779	95.7	157	1	AAP60524	Aap60524 Sequence
42	779	95.7	157	1	AAP70095	Aap70095 Tumour ne
43	779	95.7	157	1	AAP70144	Aap70144 Amino aci
44	779	95.7	157	2	AAR14270	Aar14270 Human TNF
45	779	95.7	157	2	AAR14112	Aar14112 Neutrophi

ALIGNMENTS

RESULT 1
ADH10160
ID ADH10160 standard; protein; 157 AA.
XX
AC ADH10160;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human tumour necrosis factor variant protein.
XX
KW TNF; tumour necrosis factor; polyethylene glycol; cytostatic; cancer;
KW human; variant.
XX
OS Homo sapiens.
XX
PN EP1354893-A2.
XX
PD 22-OCT-2003.
XX
PF 30-JAN-2003; 2003EP-00250587.
XX
PR 25-MAR-2002; 2002JP-00083509.
PR 26-JUN-2002; 2002JP-00185387.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (MAYU/) MAYUMI T.
PA (TSUT/) TSUTSUMI Y.
PA (NAKA/) NAKAGAWA S.
XX
PI Mayumi T, Tsutsumi Y, Nakagawa S, Ikegami H;
XX
DR WPI; 2004-063952/07.
DR N-PSDB; ADH10169.
XX
PT A physiologically active complex which comprises a protein part with
PT tumor necrosis factor activity and a high molecular part has higher
PT stability and retention in living bodies and is useful to treat disease,
PT particularly cancer.
XX
PS Example 1; SEQ ID NO 3; 18pp; English.
XX
CC The present sequence represents a physiologically active complex which
CC comprises a proteinaceous part with tumour necrosis factor (TNF) activity
CC and a high molecular part bound artificially to the N-terminus of the
CC proteinaceous part. The proteinaceous part comprises the sequence
CC selected from ADH10159 and the molecular part has a molecular weight of

```
CC   500-5000 Da and is a homopolymer of polyethylene glycol or a copolymer of
CC   ethylene glycol and its derivatives. The invention is used to treat
CC   susceptive disease, particularly cancer. The complex has a higher
CC   stability and longer retention time in living bodies than intact tumour
CC   necrosis factor. The present sequence represents a human TNF variant
CC   protein.
XX
SQ   Sequence 157 AA;

  Query Match             100.0%;  Score 814;  DB 8;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1e-75;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 2
AEB45433
ID   AEB45433 standard; protein; 157 AA.
XX
AC   AEB45433;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R1 specific human TNF-alpha mutant protein, SEQ ID No:17.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45447.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 4; SEQ ID NO 17; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R1. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             99.1%;  Score 807;  DB 9;  Length 157;
  Best Local Similarity   98.7%;  Pred. No. 5.3e-75;
  Matches  155;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||: ||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFADDGQVYFGIIAL 157


RESULT 3
AEB45432
ID   AEB45432 standard; protein; 157 AA.
XX
AC   AEB45432;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R1 specific human TNF-alpha mutant protein, SEQ ID No:16.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
```

XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (MAYU/) MAYUMI T.
PA (TSUT/) TSUTSUMI Y.
PA (NAKA/) NAKAGAWA S.
XX
PI Mayumi T, Tsutsumi Y, Nakagawa S, Ohta T;
XX
DR WPI; 2005-506850/51.
DR N-PSDB; AEB45446.
XX
PT Novel tumor necrosis factor TNF mutant protein, useful for treating
PT and/or preventing diseases such as inflammation, and other diseases
PT caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT rheumatoid arthritis, allergy.
XX
PS Claim 4; SEQ ID NO 16; 34pp; Japanese.
XX
CC The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC a TNF mutant protein comprising an amino acid sequence derived from the
CC human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC N-terminus, and amino acid residues at positions 84-89 by other amino
CC acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC protein. The TNF mutant proteins are useful for treating and/or
CC preventing diseases such as inflammation, and other diseases caused by
CC overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC represents a human TNF-alpha mutant protein specific for TNF-R1. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 157 AA;

Query Match 99.0%; Score 806; DB 9; Length 157;
Best Local Similarity 98.7%; Pred. No. 6.8e-75;
Matches 155; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
Db 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy 121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db 121 GGVFQLEPGDRLSAEINRPDYLDFRETGQVYFGIIAL 157

RESULT 4
AEB45434
ID AEB45434 standard; protein; 157 AA.
XX
AC AEB45434;
XX
DT 22-SEP-2005 (first entry)
XX
DE TNF-R1 specific human TNF-alpha mutant protein, SEQ ID No:18.
XX
KW tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW vasotropic; cerebroprotective; dermatological; immunomodulator;
KW antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2005066206-A1.
XX
PD 21-JUL-2005.
XX
PF 05-JAN-2005; 2005WO-JP000032.
XX
PR 06-JAN-2004; 2004JP-00001427.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (MAYU/) MAYUMI T.
PA (TSUT/) TSUTSUMI Y.
PA (NAKA/) NAKAGAWA S.
XX
PI Mayumi T, Tsutsumi Y, Nakagawa S, Ohta T;
XX
DR WPI; 2005-506850/51.
DR N-PSDB; AEB45448.
XX
PT Novel tumor necrosis factor TNF mutant protein, useful for treating
PT and/or preventing diseases such as inflammation, and other diseases
PT caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT rheumatoid arthritis, allergy.
XX
PS Claim 4; SEQ ID NO 18; 34pp; Japanese.
XX
CC The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC a TNF mutant protein comprising an amino acid sequence derived from the
CC human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC N-terminus, and amino acid residues at positions 84-89 by other amino
CC acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC protein. The TNF mutant proteins are useful for treating and/or
CC preventing diseases such as inflammation, and other diseases caused by
CC overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC represents a human TNF-alpha mutant protein specific for TNF-R1. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 157 AA;

Query Match 98.9%; Score 805; DB 9; Length 157;
Best Local Similarity 98.7%; Pred. No. 8.6e-75;
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
Db 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy 121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

```
                ||||||||||||||||||||||||  ||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFANDGQVYFGIIAL 157


RESULT 5
AEB45430
ID   AEB45430 standard; protein; 157 AA.
XX
AC   AEB45430;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R1 specific human TNF-alpha mutant protein, SEQ ID No:14.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45444.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 4; SEQ ID NO 14; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R1. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             98.6%;  Score 803;  DB 9;  Length 157;
  Best Local Similarity   98.1%;  Pred. No. 1.4e-74;
  Matches  154;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||| ::||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFKDTGQVYFGIIAL 157


RESULT 6
AEB45453
ID   AEB45453 standard; protein; 157 AA.
XX
AC   AEB45453;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R2 specific human TNF-alpha mutant protein, SEQ ID No:37.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45476.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 5; SEQ ID NO 37; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
```

CC human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC N-terminus, and amino acid residues at positions 84-89 by other amino
CC acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC protein. The TNF mutant proteins are useful for treating and/or
CC preventing diseases such as inflammation, and other diseases caused by
CC overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC represents a human TNF-alpha mutant protein specific for TNF-R2. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 157 AA;

Query Match 98.3%; Score 800; DB 9; Length 157;
Best Local Similarity 98.7%; Pred. No. 2.8e-74;
Matches 155; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWQNRWANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
Db 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy 121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db 121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

RESULT 7
AEB45431
ID AEB45431 standard; protein; 157 AA.
XX
AC AEB45431;
XX
DT 22-SEP-2005 (first entry)
XX
DE TNF-R1 specific human TNF-alpha mutant protein, SEQ ID No:15.
XX
KW tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW vasotropic; cerebroprotective; dermatological; immunomodulator;
KW antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2005066206-A1.
XX
PD 21-JUL-2005.
XX
PF 05-JAN-2005; 2005WO-JP000032.
XX
PR 06-JAN-2004; 2004JP-00001427.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (MAYU/) MAYUMI T.
PA (TSUT/) TSUTSUMI Y.
PA (NAKA/) NAKAGAWA S.
XX
PI Mayumi T, Tsutsumi Y, Nakagawa S, Ohta T;
XX
DR WPI; 2005-506850/51.
DR N-PSDB; AEB45445.
XX
PT Novel tumor necrosis factor TNF mutant protein, useful for treating
PT and/or preventing diseases such as inflammation, and other diseases
PT caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT rheumatoid arthritis, allergy.
XX
PS Claim 4; SEQ ID NO 15; 34pp; Japanese.
XX
CC The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC a TNF mutant protein comprising an amino acid sequence derived from the
CC human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC N-terminus, and amino acid residues at positions 84-89 by other amino
CC acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC protein. The TNF mutant proteins are useful for treating and/or
CC preventing diseases such as inflammation, and other diseases caused by
CC overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC represents a human TNF-alpha mutant protein specific for TNF-R1. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 157 AA;

Query Match 98.2%; Score 799; DB 9; Length 157;
Best Local Similarity 98.1%; Pred. No. 3.6e-74;
Matches 154; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
Db 61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy 121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db 121 GGVFQLEPGDRLSAEINRPDYLDFRTDGQVYFGIIAL 157

RESULT 8
AEB45454
ID AEB45454 standard; protein; 157 AA.
XX
AC AEB45454;
XX
DT 22-SEP-2005 (first entry)
XX
DE TNF-R2 specific human TNF-alpha mutant protein, SEQ ID No:38.
XX
KW tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW vasotropic; cerebroprotective; dermatological; immunomodulator;
KW antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;

```
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45477.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 5; SEQ ID NO 38; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R2. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.7%;  Score 795;  DB 9;  Length 157;
  Best Local Similarity   98.1%;  Pred. No. 9.3e-74;
  Matches  154;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||| |  ||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWTNGYANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 9
AEB45469
ID   AEB45469 standard; protein; 157 AA.
XX
AC   AEB45469;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R2 specific human TNF-alpha mutant protein, SEQ ID No:53.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45492.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 5; SEQ ID NO 53; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R2. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.4%;  Score 793;  DB 9;  Length 157;
```

```
  Best Local Similarity   97.5%;  Pred. No. 1.5e-73;
  Matches  153;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||||||||||||||||||||||  ||  ||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRITKSYSKPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 10
AEB45438
ID   AEB45438 standard; protein; 157 AA.
XX
AC   AEB45438;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R1 specific human TNF-alpha mutant protein, SEQ ID No:22.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45452.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 4; SEQ ID NO 22; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R1. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.3%;  Score 792;  DB 9;  Length 157;
  Best Local Similarity   97.5%;  Pred. No. 1.9e-73;
  Matches  153;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||||||||||||||||||||||  ||  ||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRIGGPYQRPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 11
AEB45436
ID   AEB45436 standard; protein; 157 AA.
XX
AC   AEB45436;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R1 specific human TNF-alpha mutant protein, SEQ ID No:20.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45450.
```

```
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 4; SEQ ID NO 20; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R1. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.3%;  Score 792;  DB 9;  Length 157;
  Best Local Similarity   97.5%;  Pred. No. 1.9e-73;
  Matches  153;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||||||||||||||||||||||  |  ||||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRIAPGYSHPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 12
AEB45461
ID   AEB45461 standard; protein; 157 AA.
XX
AC   AEB45461;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R2 specific human TNF-alpha mutant protein, SEQ ID No:45.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45484.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 5; SEQ ID NO 45; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R2. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.3%;  Score 792;  DB 9;  Length 157;
  Best Local Similarity   96.8%;  Pred. No. 1.9e-73;
  Matches  152;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||||||||||||||||||||: :| :||||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRISSAYASPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 13
AEB45460
ID   AEB45460 standard; protein; 157 AA.
XX
AC   AEB45460;
XX
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DT   22-SEP-2005  (first entry)
XX
DE   TNF-R2 specific human TNF-alpha mutant protein, SEQ ID No:44.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45483.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 5; SEQ ID NO 44; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R2. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.2%;  Score 791;  DB 9;  Length 157;
  Best Local Similarity   96.8%;  Pred. No. 2.4e-73;
  Matches  152;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||||||||||||||||||||: :|  ||||||||||||||||||||||||||||||||

Db         61 QVLFSGQGCPSTHVLLTHTISRISYNYNGPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||

Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 14
AEB45464
ID   AEB45464 standard; protein; 157 AA.
XX
AC   AEB45464;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R2 specific human TNF-alpha mutant protein, SEQ ID No:48.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45487.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 5; SEQ ID NO 48; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
```

```
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R2. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.2%;  Score 791;  DB 9;  Length 157;
  Best Local Similarity   96.8%;  Pred. No. 2.4e-73;
  Matches  152;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              ||||||||||||||||||||||  :|  ||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRITTAYSGPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 15
AEB45472
ID   AEB45472 standard; protein; 157 AA.
XX
AC   AEB45472;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R2 specific human TNF-alpha mutant protein, SEQ ID No:56.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   N-PSDB; AEB45495.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Claim 5; SEQ ID NO 56; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents a human TNF-alpha mutant protein specific for TNF-R2. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 157 AA;

  Query Match             97.1%;  Score 790;  DB 9;  Length 157;
  Best Local Similarity   96.8%;  Pred. No. 3e-73;
  Matches  152;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDMPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120
              |||||||||||||||||||||||: :|  ||||||||||||||||||||||||||||||
Db         61 QVLFSGQGCPSTHVLLTHTISRISKTYSHPVNLLSAIRSPCQRETPEGAEANPWYEPIYL 120

Qy        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||||||||||||||||||||||||||||||||
Db        121 GGVFQLEPGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


Search completed: September 16, 2006, 09:45:13
Job time : 196 secs
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OM protein - protein search, using sw model

Run on: September 19, 2006, 17:55:54 ; Search time 196 Seconds
(without alignments)
366.240 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 786
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	786	100.0	157	1	AAP60524	Aap60524 Sequence
2	786	100.0	157	1	AAP70095	Aap70095 Tumour ne
3	786	100.0	157	1	AAP70144	Aap70144 Amino aci
4	786	100.0	157	2	AAR14270	Aar14270 Human TNF
5	786	100.0	157	2	AAR14112	Aar14112 Neutrophi
6	786	100.0	157	2	AAR27747	Aar27747 Human tum
7	786	100.0	157	2	AAR42679	Aar42679 Human Tum
8	786	100.0	157	2	AAR38069	Aar38069 Human TNF
9	786	100.0	157	2	AAR62463	Aar62463 Tumour ne
10	786	100.0	157	2	AAR62466	Aar62466 Tumour ne
11	786	100.0	157	2	AAR62465	Aar62465 Tumour ne
12	786	100.0	157	2	AAR60243	Aar60243 Human TNF
13	786	100.0	157	2	AAR57437	Aar57437 Human tum
14	786	100.0	157	2	AAW28530	Aaw28530 Human TNF
15	786	100.0	157	2	AAW40819	Aaw40819 Human tum
16	786	100.0	157	2	ABB08912	Abb08912 Human tum
17	786	100.0	157	2	AAY23242	Aay23242 Human tum
18	786	100.0	157	4	AAG79124	Aag79124 Amino aci
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22	786	100.0	157	5	AAE18373	Aae18373 Human mat
23	786	100.0	157	5	AAM51166	Aam51166 Tumour ne
24	786	100.0	157	5	ABB76561	Abb76561 Human tum
25	786	100.0	157	5	ABG70571	Abg70571 Human tum
26	786	100.0	157	5	ABP54869	Abp54869 Human tum
27	786	100.0	157	5	AAB47940	Aab47940 Human tum
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36	786	100.0	157	7	ADC61354	Adc61354 Human TNF
37	786	100.0	157	7	ADC81608	Adc81608 Human tum
38	786	100.0	157	7	ADD44654	Add44654 Human tum
39	786	100.0	157	7	ADD89878	Add89878 Human tum
40	786	100.0	157	7	ADE06773	Ade06773 Human ant
41	786	100.0	157	7	ABW02400	Abw02400 Human tum
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43	786	100.0	157	7	ABW02035	Abw02035 Human tum
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46	786	100.0	157	7	ABW02652	Abw02652 Human mat
47	786	100.0	157	7	ADJ63985	Adj63985 Recombina
48	786	100.0	157	7	ADM15642	Adm15642 Human tum
49	786	100.0	157	7	ADM83147	Adm83147 Human tum
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79	786	100.0	158	1	AAP91026	Aap91026 Human tum
80	786	100.0	158	1	AAP93188	Aap93188 Synthetic
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83	786	100.0	158	2	AAR07901	Aar07901 Human TNF
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95	786	100.0	164	6	ABR42163	Abr42163 His-tagge
96	786	100.0	164	9	ADZ56235	Adz56235 Histidine

97	786	100.0	164	9	AEC10124	Aec10124 Human TNF
98	786	100.0	164	9	AED95307	Aed95307 His-tagge
99	786	100.0	170	6	ADA00722	Ada00722 Human TNF
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103	786	100.0	193	2	AAW48246	Aaw48246 Tumour ne
104	786	100.0	193	2	AAW90067	Aaw90067 Human TNF
105	786	100.0	193	5	ABG73877	Abg73877 FLAG tagg
106	786	100.0	193	5	AAM50621	Aam50621 Tumour ne
107	786	100.0	193	7	ADC28285	Adc28285 Peptide t
108	786	100.0	232	7	ABW02665	Abw02665 Human pro
109	786	100.0	233	1	AAP50096	Aap50096 Sequence
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122	786	100.0	233	2	AAR97383	Aar97383 Human tum
123	786	100.0	233	2	AAW00454	Aaw00454 Human tum
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125	786	100.0	233	3	AAB37798	Aab37798 Human TNF
126	786	100.0	233	4	AAB74363	Aab74363 Human tum
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149	786	100.0	233	7	ABW02644	Abw02644 Human pro
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153	786	100.0	233	8	ADF90411	Adf90411 Human tum
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155	786	100.0	233	8	ADL23574	Adl23574 Human tum
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162	786	100.0	233	8	ADR44812	Adr44812 Tumour ne
163	786	100.0	233	8	ADR45571	Adr45571 Homologue
164	786	100.0	233	8	ADR47160	Adr47160 Human tum
165	786	100.0	233	8	ADT08161	Adt08161 Human tum
166	786	100.0	233	8	ADT78391	Adt78391 Human TNF
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171	786	100.0	233	9	ADZ26521	Adz26521 Human TNF
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180	786	100.0	514	6	AAO30491	Aao30491 Human TNF
181	786	100.0	514	6	AAO30490	Aao30490 Human TNF
182	786	100.0	514	6	AAO30495	Aao30495 Human TNF
183	786	100.0	517	6	AAO30492	Aao30492 Human TNF
184	786	100.0	584	4	AAB83212	Aab83212 Single ch
185	786	100.0	597	5	AAE18377	Aae18377 Human N-t
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187	786	100.0	652	2	AAW48650	Aaw48650 Heavy cha
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191	783	99.6	158	1	AAP70636	Aap70636 Sequence
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194	783	99.6	177	1	AAP60417	Aap60417 Human tum
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196	782	99.5	157	2	AAR14897	Aar14897 Antitumou
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200	782	99.5	157	2	AAR62467	Aar62467 Tumour ne

ALIGNMENTS

RESULT 1
AAP60524
ID AAP60524 standard; protein; 157 AA.
XX
AC AAP60524;
XX
DT 25-MAR-2003 (revised)
DT 07-AUG-1991 (first entry)
XX
DE Sequence of tumour necrosis factor (TNF).
XX
KW Anticancer agent; antitumour; antimalarial; tumour necrosis factor.
XX
OS Oryctolagus cuniculus.
XX
PN WO8603751-A.
XX
PD 03-JUL-1986.
XX
PF 19-DEC-1985; 85WO-EP000721.
XX
PR 21-DEC-1984; 84US-00684595.
PR 09-OCT-1985; 85US-00785847.
PR 09-OCT-1986; 86WO-US002133.
XX
PA (BIOJ) BIOGEN NV.
PA (FIER/) FIERS W C.
PA (ALLE/) ALLET B.
PA (BIOJ) BIOGEN INC.
XX
PI Fiers WC, Fransen LM, Tavernier JHL, Marmenout ALM, Vanderheyd J;
PI Allet B;
XX
DR WPI; 1986-182891/28.
DR N-PSDB; AAN60442.
XX
PT Mammalian tumour necrosis factors - produced by culturing pro-karyotic

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 19, 2006, 18:05:19 ; Search time 50 Seconds
(without alignments)
274.846 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 786
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	786	100.0	157	1	US-07-794-400-1	Sequence 1, Appli
2	786	100.0	157	1	US-08-041-648-2	Sequence 2, Appli
3	786	100.0	157	1	US-08-107-235-1	Sequence 1, Appli
4	786	100.0	157	1	US-08-217-529-2	Sequence 2, Appli
5	786	100.0	157	1	US-08-318-193-86	Sequence 86, Appl
6	786	100.0	157	1	US-08-397-470-1	Sequence 1, Appli
7	786	100.0	157	1	US-08-192-102-1	Sequence 1, Appli
8	786	100.0	157	1	US-08-324-799-1	Sequence 1, Appli
9	786	100.0	157	1	US-08-538-875-1	Sequence 1, Appli
10	786	100.0	157	1	US-08-394-600B-17	Sequence 17, Appl
11	786	100.0	157	1	US-08-500-860A-35	Sequence 35, Appl
12	786	100.0	157	1	US-08-192-861A-1	Sequence 1, Appli
13	786	100.0	157	1	US-08-600-783-5	Sequence 5, Appli
14	786	100.0	157	2	US-08-584-031-13	Sequence 13, Appl
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16	786	100.0	157	2	US-09-133-119-1	Sequence 1, Appli
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19	786	100.0	157	2	US-09-496-118B-7	Sequence 7, Appli
20	786	100.0	157	2	US-08-395-456C-17	Sequence 17, Appl
21	786	100.0	157	2	US-08-487-453A-17	Sequence 17, Appl
22	786	100.0	157	2	US-09-582-450-13	Sequence 13, Appl
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38	786	100.0	193	1	US-08-889-909A-3	Sequence 3, Appli
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62	786	100.0	233	3	US-10-040-281A-20	Sequence 20, Appl
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66	784	99.7	157	1	US-07-940-605A-5	Sequence 5, Appli
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70	782	99.5	231	2	US-08-815-783-5	Sequence 5, Appli
71	781	99.4	158	1	US-07-794-400-6	Sequence 6, Appli
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73	781	99.4	158	1	US-07-794-400-8	Sequence 8, Appli
74	781	99.4	158	1	US-08-397-470-6	Sequence 6, Appli
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76	781	99.4	158	1	US-08-397-470-8	Sequence 8, Appli
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ALIGNMENTS

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; Patent No. 5422104
;  GENERAL INFORMATION:
;    APPLICANT:  Fiers, W.
;    APPLICANT:  Tavernier, J.
;    APPLICANT:  Van Ostade, X.
;    TITLE OF INVENTION:  TNF-Muteins
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,400
;      FILING DATE:  19911120
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 90810901.0
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Krovatin, William
;      REGISTRATION NUMBER:  33256
;      REFERENCE/DOCKET NUMBER:  4105/136-00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4387
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  AMINO ACID
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GenCore version 5.1.9

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(without alignments)
399.586 Million cell updates/sec

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Perfect score: 786
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Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT APPLICATION NUMBER: US/09/756,301A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S.07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
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GenCore version 5.1.9

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Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	786	100.0	157	7	US-11-143-926-1	Sequence 1, Appli
3	786	100.0	157	7	US-11-314-941-1	Sequence 1, Appli
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6	786	100.0	233	7	US-11-382-837-3	Sequence 3, Appli
7	786	100.0	233	7	US-11-377-165A-3	Sequence 3, Appli
8	777	98.9	233	7	US-11-337-690-5	Sequence 5, Appli
9	755	96.1	150	7	US-11-315-825-28	Sequence 28, Appl
10	755	96.1	152	6	US-10-794-755-5	Sequence 5, Appli
11	755	96.1	152	6	US-10-527-832-6	Sequence 6, Appli
12	641.5	81.6	235	7	US-11-241-106-8	Sequence 8, Appli
13	217.5	27.7	147	6	US-10-794-755-6	Sequence 6, Appli
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16	217.5	27.7	205	7	US-11-377-165A-4	Sequence 4, Appli
17	215.5	27.4	205	7	US-11-337-690-6	Sequence 6, Appli
18	214	27.2	51	6	US-10-978-053C-1	Sequence 1, Appli
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26	169.5	21.6	179	6	US-10-861-934-22	Sequence 22, Appl
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36	163	20.7	276	7	US-11-015-117-49	Sequence 49, Appl
37	163	20.7	281	6	US-10-511-937-2473	Sequence 2473, Ap
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39	163	20.7	281	6	US-10-861-934-30	Sequence 30, Appl
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44	163	20.7	282	7	US-11-015-117-48	Sequence 48, Appl
45	161	20.5	178	6	US-10-861-934-84	Sequence 84, Appl
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50	158.5	20.2	138	6	US-10-861-934-81	Sequence 81, Appl
51	158.5	20.2	139	6	US-10-861-934-80	Sequence 80, Appl
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53	158.5	20.2	141	6	US-10-861-934-79	Sequence 79, Appl
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62	127	16.2	316	7	US-11-241-106-4	Sequence 4, Appli
63	126	16.0	172	6	US-10-669-920-179	Sequence 179, App
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65	126	16.0	244	6	US-10-669-920-177	Sequence 177, App
66	126	16.0	311	6	US-10-669-920-181	Sequence 181, App
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150	71.5	9.1	431	7	US-11-330-403-7623	Sequence 7623, Ap
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152	71.5	9.1	554	7	US-11-330-403-4081	Sequence 4081, Ap
153	71	9.0	271	6	US-10-953-349-26860	Sequence 26860, A
154	71	9.0	271	7	US-11-056-355B-68802	Sequence 68802, A
155	71	9.0	322	6	US-10-953-349-26859	Sequence 26859, A
156	71	9.0	322	7	US-11-056-355B-68801	Sequence 68801, A
157	71	9.0	435	6	US-10-953-349-2231	Sequence 2231, Ap
158	71	9.0	435	7	US-11-056-355B-35337	Sequence 35337, A
159	71	9.0	435	7	US-11-056-355B-102962	Sequence 102962,
160	71	9.0	435	7	US-11-056-355B-114201	Sequence 114201,
161	71	9.0	518	7	US-11-293-697-4439	Sequence 4439, Ap
162	71	9.0	571	6	US-10-953-349-2230	Sequence 2230, Ap
163	71	9.0	571	7	US-11-056-355B-35336	Sequence 35336, A
164	71	9.0	571	7	US-11-056-355B-102961	Sequence 102961,
165	71	9.0	571	7	US-11-056-355B-114200	Sequence 114200,
166	71	9.0	576	6	US-10-953-349-2229	Sequence 2229, Ap
167	71	9.0	576	7	US-11-056-355B-35335	Sequence 35335, A
168	71	9.0	576	7	US-11-056-355B-102960	Sequence 102960,
169	71	9.0	576	7	US-11-056-355B-114199	Sequence 114199,
170	70.5	9.0	210	7	US-11-056-355B-102587	Sequence 102587,
171	70.5	9.0	210	7	US-11-056-355B-113826	Sequence 113826,
172	70.5	9.0	257	7	US-11-056-355B-102586	Sequence 102586,
173	70.5	9.0	257	7	US-11-056-355B-113825	Sequence 113825,
174	70.5	9.0	310	7	US-11-056-355B-102585	Sequence 102585,
175	70.5	9.0	310	7	US-11-056-355B-113824	Sequence 113824,
176	70.5	9.0	311	7	US-11-056-355B-51743	Sequence 51743, A
177	70.5	9.0	345	7	US-11-056-355B-51742	Sequence 51742, A
178	70.5	9.0	352	7	US-11-056-355B-103385	Sequence 103385,
179	70.5	9.0	352	7	US-11-056-355B-114624	Sequence 114624,
180	70.5	9.0	392	7	US-11-056-355B-51741	Sequence 51741, A
181	70.5	9.0	435	6	US-10-953-349-17331	Sequence 17331, A
182	70.5	9.0	471	7	US-11-330-403-3830	Sequence 3830, Ap
183	70.5	9.0	513	6	US-10-953-349-17330	Sequence 17330, A
184	70.5	9.0	525	6	US-10-953-349-17329	Sequence 17329, A
185	70	8.9	398	6	US-10-449-902-38237	Sequence 38237, A
186	70	8.9	768	7	US-11-056-355B-72719	Sequence 72719, A
187	70	8.9	806	7	US-11-056-355B-70758	Sequence 70758, A
188	70	8.9	806	7	US-11-056-355B-72718	Sequence 72718, A
189	70	8.9	818	7	US-11-056-355B-70757	Sequence 70757, A
190	70	8.9	818	7	US-11-056-355B-72717	Sequence 72717, A
191	70	8.9	822	7	US-11-056-355B-70756	Sequence 70756, A
192	69.5	8.8	807	7	US-11-293-697-2725	Sequence 2725, Ap
193	69.5	8.8	886	6	US-10-449-902-43638	Sequence 43638, A
194	69.5	8.8	886	6	US-10-449-902-46619	Sequence 46619, A
195	69	8.8	275	6	US-10-449-902-43001	Sequence 43001, A
196	69	8.8	406	7	US-11-122-986-104	Sequence 104, App
197	69	8.8	406	7	US-11-122-986-106	Sequence 106, App
198	69	8.8	433	7	US-11-330-403-14921	Sequence 14921, A
199	69	8.8	523	7	US-11-330-403-15865	Sequence 15865, A
200	69	8.8	532	7	US-11-330-403-18247	Sequence 18247, A

ALIGNMENTS

RESULT 1
US-11-297-810-1
; Sequence 1, Application US/11297810
; Publication No. US20060121037A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghrayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of Human
; TITLE OF INVENTION: Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-049
; CURRENT APPLICATION NUMBER: US/11/297,810
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: U.S. 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S.08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: September 19, 2006, 18:00:19 ; Search time 39 Seconds
(without alignments)
387.334 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 786
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	786	100.0	233	1	QWHUN	tumor necrosis fac
2	779	99.1	233	1	S22052	tumor necrosis fac
3	718	91.3	233	2	S11688	tumor necrosis fac
4	704	89.6	234	1	JQ1344	tumor necrosis fac
5	685.5	87.2	232	1	S12606	tumor necrosis fac
6	641.5	81.6	235	1	QWMSN	tumor necrosis fac
7	639	81.3	185	2	S52715	tumor necrosis fac
8	639	81.3	233	1	S24642	tumor necrosis fac
9	638.5	81.2	234	1	A25451	tumor necrosis fac
10	637	81.0	234	1	JH0529	tumor necrosis fac
11	635.5	80.9	235	2	I54490	tumor necrosis fac
12	632.5	80.5	193	2	S06192	tumor necrosis fac
13	626.5	79.7	235	2	JU0029	tumor necrosis fac
14	260.5	33.1	197	1	JH0309	tumor necrosis fac
15	253.5	32.3	204	1	S24641	lymphotoxin - bovi
16	249.5	31.7	204	1	S17289	tumor necrosis fac
17	243	30.9	202	1	JN0869	tumor necrosis fac
18	240.5	30.6	202	1	B27303	tumor necrosis fac
19	217.5	27.7	205	1	QWHUX	lymphotoxin alpha
20	177	22.5	244	2	A46066	lymphotoxin beta -
21	176.5	22.5	278	2	A49266	fas ligand - rat
22	169.5	21.6	279	2	A53062	Fas ligand - mouse
23	163	20.7	281	2	I38707	Fas ligand - human
24	150	19.1	306	2	I49139	lymphotoxin-beta -
25	131.5	16.7	260	2	S21738	CD40 ligand - mous
26	120	15.3	261	2	I53476	CD40 ligand - huma
27	119	15.1	261	2	S53090	CD40 ligand - bovi
28	81.5	10.4	887	2	AD2009	hypothetical prote
29	81	10.3	265	2	B84108	hypothetical prote
30	80	10.2	286	2	S56436	hypothetical 29.7K
31	80	10.2	799	2	C82929	ATP synthase alpha
32	80	10.2	1369	2	D86178	hypothetical prote
33	79.5	10.1	4077	2	T17484	hypothetical prote
34	79	10.1	286	2	E91277	probable oxidoredu
35	79	10.1	286	2	E86118	probable oxidoredu
36	78.5	10.0	385	2	AH2269	heterocyst specifi
37	78	9.9	234	2	A40710	CD30 ligand - huma
38	78	9.9	260	2	T30236	methyltransferase
39	78	9.9	476	2	H82177	conserved hypothet
40	78	9.9	601	2	T49752	hypothetical prote
41	78	9.9	724	2	A53371	glutamate-ammonia
42	78	9.9	1560	2	T09202	probable tail comp
43	77	9.8	1680	1	C5MS	complement C5 prec
44	76.5	9.7	479	2	F70965	hypothetical prote
45	76	9.7	167	2	B71553	hypothetical prote
46	76	9.7	993	2	G84632	hypothetical prote
47	75.5	9.6	217	2	F86343	hypothetical prote
48	75	9.5	193	2	A40738	surface antigen CD
49	75	9.5	466	2	AC3206	two component sens
50	75	9.5	468	2	AC3595	UDP-N-acetylglucos
51	74.5	9.5	288	2	A83443	probable transcrip
52	74.5	9.5	352	2	T51835	3-methyl-2-oxobuta
53	74.5	9.5	356	2	T30361	occlusion-derived
54	74.5	9.5	403	2	I54192	aminomethyltransfe
55	74.5	9.5	430	2	AG2256	dihydrolipoamide S
56	74	9.4	230	2	A95354	probable GntR-fami
57	74	9.4	357	2	B83652	hypothetical prote
58	74	9.4	528	2	D90545	atp synthase alpha
59	74	9.4	1083	2	H86921	probable arabinosy
60	73.5	9.4	264	2	AE2100	phosphonate ABC tr
61	73.5	9.4	473	2	B70541	hypothetical prote
62	73	9.3	239	2	B40710	CD30 ligand - mous
63	73	9.3	292	2	T33987	hypothetical prote
64	73	9.3	447	2	S37844	molybdopterin-conv
65	73	9.3	675	2	E75393	hypothetical prote
66	72.5	9.2	213	2	AF2283	hypothetical prote
67	72.5	9.2	229	2	B82669	conserved hypothet
68	72.5	9.2	350	2	JQ1656	ethylene-forming e
69	72.5	9.2	499	2	F86645	amidase (imported)
70	72.5	9.2	506	2	B87102	conserved membrane
71	72.5	9.2	614	2	T10862	phaseolin G-box bi
72	72.5	9.2	774	1	QRECFA	iron(III) dicitrat
73	72.5	9.2	818	1	JC4397	peroxinectin precu
74	72.5	9.2	863	2	F84504	probable retroelem
75	72	9.2	437	2	F83854	hypothetical prote
76	72	9.2	457	2	T24962	odr-7 protein - Ca
77	72	9.2	504	1	S23558	ubiquinol-cytochro
78	72	9.2	570	2	T11647	probable pyruvate
79	72	9.2	632	2	AE3560	proline/betaine tr
80	72	9.2	882	2	AF3036	nitrate reductase
81	72	9.2	903	2	E98249	nitrate reductase
82	72	9.2	4342	2	H83343	probable non-ribos
83	71.5	9.1	157	2	S65055	coat protein - Chi
84	71.5	9.1	312	2	AD0779	conserved hypothet
85	71.5	9.1	402	2	A87492	glycosyl transfera
86	71.5	9.1	475	2	D83202	alginate biosynthe
87	71.5	9.1	692	2	H69416	conserved hypothet
88	71.5	9.1	750	2	S75636	sensory transducti
89	71	9.0	387	2	JC2484	xylan endo-1,3-bet
90	71	9.0	511	2	T26124	hypothetical prote
91	71	9.0	890	2	E84846	probable receptor-
92	71	9.0	1176	2	S40899	VPS8 protein - yea
93	71	9.0	1230	2	S53974	hypothetical prote
94	71	9.0	1626	2	T09271	probable tail comp
95	70.5	9.0	153	2	S50431	hypothetical prote
96	70.5	9.0	175	2	AE3293	hypothetical prote
97	70.5	9.0	262	2	G87555	hypothetical prote
98	70.5	9.0	310	2	F96641	hypothetical prote
99	70.5	9.0	324	2	H82681	integrase/recombin
100	70.5	9.0	352	2	D96597	hypothetical prote
101	70.5	9.0	513	2	T05948	cytochrome P450 77
102	70.5	9.0	563	2	T20631	hypothetical prote

103	70.5	9.0	573	2	F89719	protein F09B12.1 [
104	70.5	9.0	573	2	T20632	hypothetical prote
105	70.5	9.0	710	2	G82689	soluble lytic mure
106	70.5	9.0	756	2	A43582	surface antigen ms
107	70.5	9.0	1123	2	AB0125	exodeoxyribonuclea
108	70.5	9.0	3144	2	S64791	VPS13 protein - ye
109	70	8.9	157	2	S48701	coat protein, 18K
110	70	8.9	195	2	S44788	D2007.2 protein -
111	70	8.9	393	1	TVBE66	protein kinase (EC
112	70	8.9	413	2	T04520	hypothetical prote
113	70	8.9	514	2	T15944	hypothetical prote
114	70	8.9	533	2	B83813	catalase katX [imp
115	70	8.9	822	2	T48570	hypothetical prote
116	70	8.9	872	2	S49541	cellulase - Cellul
117	70	8.9	904	2	T40072	P Type Copper ATPa
118	70	8.9	976	2	D96714	DNA-directed RNA p
119	69.5	8.8	335	2	AG2311	hypothetical prote
120	69.5	8.8	342	2	AF3357	anthranilate phosp
121	69.5	8.8	367	2	G83309	conserved hypothet
122	69.5	8.8	469	2	G69267	conserved hypothet
123	69.5	8.8	482	2	A70963	hypothetical prote
124	69.5	8.8	500	2	I56502	4-aminobutyrate tr
125	69.5	8.8	563	2	S77533	DNA mismatch repai
126	69.5	8.8	581	2	T23396	hypothetical prote
127	69.5	8.8	641	2	F71810	type III DNA modif
128	69.5	8.8	3603	1	D69681	peptide synthetase
129	69.5	8.8	3972	2	S75251	hypothetical prote
130	69	8.8	285	2	AH0200	conserved hypothet
131	69	8.8	303	2	T00899	hypothetical prote
132	69	8.8	357	2	T20029	hypothetical prote
133	69	8.8	406	2	H83074	GTP-binding protei
134	69	8.8	434	2	S74706	(S)-2-hydroxy-acid
135	69	8.8	466	2	AH3100	amidohydrolase [im
136	69	8.8	466	2	B98186	probable hydrolase
137	69	8.8	505	2	G97252	foF1-type ATP synt
138	69	8.8	532	2	T30764	hypothetical prote
139	69	8.8	540	2	S63299	sugar transport pr
140	69	8.8	708	2	AG2315	hypothetical prote
141	69	8.8	1136	2	T30878	dynein heavy chain
142	69	8.8	1365	2	A41483	glucosyltransferas
143	69	8.8	1377	2	E86034	rhsA protein in rh
144	69	8.8	1377	2	C65159	rhsA protein precu
145	69	8.8	1394	2	H91236	RhsH core protein
146	69	8.8	1397	2	A85570	rhsC protein in rh
147	69	8.8	1397	2	C64805	rhsC protein precu
148	69	8.8	1397	2	T46354	hypothetical prote
149	69	8.8	1399	2	A99720	RhsC core protein
150	69	8.8	1409	2	F91187	rhsA core protein
151	69	8.8	1411	2	E65145	rhsB protein precu
152	69	8.8	2548	2	E59435	myosin IXA [import
153	69	8.8	2626	2	T31099	myosin-RhoGAP prot
154	68.5	8.7	206	2	G82893	urease complex com
155	68.5	8.7	232	2	AG2876	RNA methylase [imp
156	68.5	8.7	261	2	S24418	dmpE protein - Pse
157	68.5	8.7	285	2	A97653	probable rRNA meth
158	68.5	8.7	295	2	C95285	probable LysR-type
159	68.5	8.7	438	2	E75112	asparaginase (asna
160	68.5	8.7	479	2	C90457	cytochrome b558/56
161	68.5	8.7	501	2	S28592	cypro4 protein - c
162	68.5	8.7	613	2	T43933	DNA-directed DNA p
163	68.5	8.7	667	2	S74254	homeotic protein s
164	68.5	8.7	752	2	E72616	hypothetical prote
165	68.5	8.7	1149	2	S67099	DNA-directed RNA p
166	68.5	8.7	1275	2	D38164	cobN protein - Pse
167	68.5	8.7	7463	2	T36248	CDA peptide synthe
168	68	8.7	235	2	JC2322	hypothetical 26.8K
169	68	8.7	256	2	B82076	probable general s
170	68	8.7	266	2	C72669	probable serine/th
171	68	8.7	471	2	S29039	Na+-transporting A
172	68	8.7	484	2	T33504	hypothetical prote
173	68	8.7	494	2	F70981	probable aldehyde
174	68	8.7	532	2	B82102	membrane-bound lyt
175	68	8.7	666	2	H75295	transketolase - De
176	68	8.7	1159	2	I38465	probable potassium
177	68	8.7	2869	2	T18518	apolipoprotein(a)
178	68	8.7	6420	2	T30283	polyketide synthas
179	67.5	8.6	143	2	D84318	hypothetical prote
180	67.5	8.6	185	2	S21366	actin-binding prot
181	67.5	8.6	203	2	G86785	acetyltransferase
182	67.5	8.6	339	1	R6BY13	ribosomal protein
183	67.5	8.6	400	2	A39254	inositol-1,4-bisph
184	67.5	8.6	406	2	T30650	hypothetical prote
185	67.5	8.6	459	2	F83602	hypothetical prote
186	67.5	8.6	473	2	A03959	pol polyprotein -
187	67.5	8.6	498	2	A72725	probable beta-lact
188	67.5	8.6	550	2	G84500	hypothetical prote
189	67.5	8.6	625	2	H84863	hypothetical prote
190	67.5	8.6	740	2	D95191	GTP pyrophosphokin
191	67.5	8.6	740	2	F98057	GTP diphosphokinas
192	67.5	8.6	758	2	B87574	NADP-dependent mal
193	67.5	8.6	873	1	JH0182	nitrate reductase
194	67.5	8.6	1012	2	T44185	probable DNA-direc
195	67.5	8.6	1012	2	T43998	DNA polymerase [im
196	67.5	8.6	1099	2	T16283	hypothetical prote
197	67.5	8.6	1336	2	T17479	hypothetical prote
198	67.5	8.6	2352	2	C83229	probable non-ribos
199	67.5	8.6	2700	2	D88450	protein F21H11.2 [
200	67	8.5	104	2	F83343	hypothetical prote

ALIGNMENTS

RESULT 1
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tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chron
A;Reference number: A93585; MUID:86016093; PMID:2995927
A;Accession: A93585
A;Molecule type: DNA
A;Residues: 1-233 <NED>
A;Cross-references: UNIPROT:P01375; UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g37
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka,
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <IRI>
A;Cross-references: UNIPARC:UPI000000D745; EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.;
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to ly
A;Reference number: A93351; MUID:85086244; PMID:6392892
A;Accession: A93351
A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Cross-references: UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA266
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc
R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
A;Accession: A44189
A;Molecule type: mRNA
A;Residues: 1-62,'S',64-233 <WAN>
A;Cross-references: UNIPARC:UPI000002FB8A; GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Anc

OM protein - protein search, using sw model

Run on: September 19, 2006, 17:56:44 ; Search time 298 Seconds
(without alignments)
487.340 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 786
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	786	100.0	233	1	TNFA_HUMAN	P01375 homo sapien
2	786	100.0	233	2	Q5STB3_HUMAN	Q5stb3 homo sapien
3	779	99.1	233	1	TNFA_PAPSP	P33620 papio sp. (
4	777	98.9	232	1	TNFA_PANTR	Q8hzd9 pan troglod
5	768	97.7	233	1	TNFA_MACMU	P48094 macaca mula
6	765	97.3	233	1	TNFA_MACFA	P79337 macaca fasc
7	764	97.2	233	1	TNFA_PAPHU	O77510 papio hamad
8	761	96.8	233	1	TNFA_PAPAN	P59695 papio anubi
9	751	95.5	149	2	O97543_AOTNA	O97543 aotus nancy
10	745	94.8	233	1	TNFA_CANFA	P51742 canis famil
11	739	94.0	233	2	Q2MJ87_TRIMA	Q2mj87 trichechus
12	737	93.8	233	1	TNFA_FELCA	P19101 felis silve
13	722	91.9	233	2	Q2LAH3_DICBI	Q2lah3 diceros bic
14	714	90.8	233	1	TNFA_SAISC	Q8mkg8 saimiri sci
15	704	89.6	234	1	TNFA_HORSE	P29553 equus cabal
16	703	89.4	149	2	O97538_AOTVO	O97538 aotus vocif
17	703	89.4	149	2	Q9TTG8_AOTNI	Q9ttg8 aotus nigri
18	698	88.8	217	2	Q9BEG0_CYCDI	Q9beg0 cyclopes di
19	694	88.3	217	2	Q9BEG1_BRATR	Q9beg1 bradypus tr
20	687	87.4	233	1	TNFA_DELLE	Q8wnr1 delphinapte
21	685.5	87.2	232	1	TNFA_PIG	P23563 sus scrofa
22	677	86.1	233	2	Q2LAH2_STEBR	Q2lah2 steno breda
23	669	85.1	233	1	TNFA_TURTR	Q9bea1 tursiops tr
24	658	83.7	217	2	Q9BEF4_CABUN	Q9bef4 cabassous u
25	650	82.7	138	2	Q9TTG7_AOTLE	Q9ttg7 aotus lemur
26	649	82.6	234	1	TNFA_CAPHI	P13296 capra hircu
27	646	82.2	234	2	Q53ZM5_CAPHI	Q53zm5 capra hircu
28	644.5	82.0	234	1	TNFA_CAVPO	P51435 cavia porce
29	642	81.7	216	2	Q9BEC4_TALEU	Q9bec4 talpa europ
30	641.5	81.6	235	1	TNFA_MOUSE	P06804 mus musculu
31	641.5	81.6	235	2	Q3U593_MOUSE	Q3u593 m 3 days ne
32	640	81.4	229	1	TNFA_CEREL	P51743 cervus elap
33	639	81.3	233	1	TNFA_BOVIN	Q06599 bos taurus
34	639	81.3	233	1	TNFA_BUBBU	P59693 bubalus bub
35	639	81.3	234	1	TNFA_BOSIN	P59684 bos indicus
36	639	81.3	234	2	Q539C2_TUPTA	Q539c2 tupaia tana
37	639	81.3	234	2	Q2MGZ7_9CETA	Q2mgz7 bubalus bub
38	639	81.3	234	2	Q2MH01_BUBBU	Q2mh01 bubalus bub
39	639	81.3	234	2	Q2MH05_9CETA	Q2mh05 bubalus car
40	638.5	81.2	235	1	TNFA_RABIT	P04924 oryctolagus
41	637	81.0	234	1	TNFA_SHEEP	P23383 ovis aries
42	635.5	80.9	235	1	TNFA_PERLE	P36939 peromyscus
43	630.5	80.2	235	2	Q5W9H9_MERUN	Q5w9h9 meriones un
44	629.5	80.1	232	2	Q80XA4_PERMA	Q80xa4 peromyscus
45	626.5	79.7	235	1	TNFA_RAT	P16599 rattus norv
46	626.5	79.7	235	2	Q6EE11_RAT	Q6eel1 rattus norv
47	620	78.9	233	1	TNFA_CAMBA	Q75n23 camelus bac
48	620	78.9	233	1	TNFA_LAMGL	P59694 lama glama
49	618.5	78.7	156	2	Q91ZL4_SIGHI	Q91zl4 sigmodon hi
50	611.5	77.8	233	1	TNFA_MARMO	O35734 marmota mon
51	611.5	77.8	233	2	Q6X658_MARMO	Q6x658 marmota mon
52	610.5	77.7	216	2	Q9BEC9_OCHPR	Q9bec9 ochotona pr
53	607	77.2	215	2	Q9BEE8_ERIEU	Q9bee8 erinaceus e
54	596.5	75.9	216	2	O70332_MESAU	O70332 mesocricetu
55	592.5	75.4	217	2	Q9ERG6_PERMA	Q9erg6 peromyscus
56	591	75.2	217	2	Q9BEC5_TENEC	Q9bec5 tenrec ecau
57	584	74.3	215	2	Q99ND1_SCIVU	Q99nd1 sciurus vul
58	584	74.3	233	1	TNFA_MACEU	O77764 macropus eu
59	584	74.3	233	2	Q3T4H5_MACEU	Q3t4h5 macropus eu
60	576.5	73.3	219	2	Q3U4I6_MOUSE	Q3u4i6 mus musculu
61	546	69.5	216	2	Q9BEE0_MACRU	Q9bee0 macropus ru
62	539	68.6	155	2	Q8HZD8_9PRIM	Q8hzd8 gorilla gor
63	538	68.4	155	2	Q8HZD7_PONPY	Q8hzd7 pongo pygma
64	509	64.8	155	2	Q8HZD5_SAGOE	Q8hzd5 saguinus oe
65	486	61.8	103	2	Q864Z0_PHYCA	Q864z0 physeter ca
66	479	60.9	103	2	Q864Y9_9EUTH	Q864y9 manis sp. c
67	464	59.0	99	2	Q864Y8_ELEMA	Q864y8 elephas max
68	460.5	58.6	214	2	Q9BEF3_DIDMA	Q9bef3 didelphis m
69	459.5	58.5	102	2	Q80Z02_9HYST	Q80z02 trichys fas
70	452.5	57.6	102	2	Q80Z03_CASCN	Q80z03 castor cana
71	452	57.5	99	2	Q95LE8_CANFA	Q95le8 canis famil
72	443.5	56.4	102	2	Q80Z04_9RODE	Q80z04 anomalurus
73	441.5	56.2	102	2	Q80Z06_DIPSA	Q80z06 dipus sagit
74	438	55.7	233	1	TNFA_TRIVU	P79374 trichosurus
75	436	55.5	103	2	Q864Y7_TUPTA	Q864y7 tupaia tana
76	404.5	51.5	102	2	Q80Z05_DIPME	Q80z05 dipodomys m
77	314	39.9	70	2	Q7YSE3_SHEEP	Q7yse3 ovis aries
78	291	37.0	101	2	Q9R136_MERUN	Q9r136 meriones un
79	274	34.9	70	2	Q75T06_RABIT	Q75t06 oryctolagus
80	271.5	34.5	175	2	Q2HZD0_PHOSU	Q2hzd0 phodopus su
81	268	34.1	65	2	Q95N81_CANFA	Q95n81 canis famil
82	265.5	33.8	205	1	TNFB_MARMO	Q9jm09 marmota mon
83	264	33.6	253	2	Q7T194_ACASC	Q7t194 acanthopagr
84	260.5	33.1	197	1	TNFB_RABIT	P10154 oryctolagus
85	259	33.0	74	2	Q6PWY4_PIG	Q6pwy4 sus scrofa
86	255	32.4	222	2	Q7T1U4_PAGMA	Q7t1u4 pagrus majo
87	253.5	32.3	204	1	TNFB_BOVIN	Q06600 bos taurus
88	253.5	32.3	204	1	TNFB_CANFA	Q5wr07 canis famil
89	251	31.9	253	1	TNFA_SPAAU	Q8jfg3 sparus aura
90	249.5	31.7	204	1	TNFB_PIG	P26445 sus scrofa
91	249	31.7	201	1	TNFB_MACEU	Q9xt48 macropus eu
92	249	31.7	201	2	Q3T4H4_MACEU	Q3t4h4 macropus eu
93	248	31.6	241	2	Q6U817_LATJA	Q6u817 lateolabrax
94	244.5	31.1	202	2	Q80WE7_PERMA	Q80we7 peromyscus
95	243.5	31.0	225	2	Q9IB42_PAROL	Q9ib42 paralichthy
96	243.5	31.0	250	2	Q4W8A0_FUGRU	Q4w8a0 fugu rubrip
97	243	30.9	202	1	TNFB_RAT	Q06332 rattus norv
98	241.5	30.7	225	2	Q9IB41_PAROL	Q9ib41 paralichthy
99	240.5	30.6	202	1	TNFB_MOUSE	P09225 mus musculu
100	240.5	30.6	202	2	Q542S2_MOUSE	Q542s2 m 3 days ne
101	234.5	29.8	247	2	Q5VJN5_ORENI	Q5vjn5 oreochromis
102	225	28.6	246	2	Q9I970_ONCMY	Q9i970 oncorhynchu
103	225	28.6	246	2	Q9I976_ONCMY	Q9i976 oncorhynchu
104	222	28.2	188	2	Q5BMN1_SALSA	Q5bmn1 salmo salar

105	222	28.2	246	2	Q5BMN3_SALSA	Q5bmn3 salmo salar
106	217.5	27.7	205	1	TNFB_HUMAN	P01374 homo sapien
107	217.5	27.7	205	1	TNFB_PANTR	P61125 pan troglod
108	217.5	27.7	205	2	Q5STV3_HUMAN	Q5stv3 homo sapien
109	217.5	27.7	205	2	Q6FG55_HUMAN	Q6fg55 homo sapien
110	217.5	27.7	205	2	Q5ST95_HUMAN	Q5st95 homo sapien
111	216.5	27.5	205	1	TNFB_MACMU	Q5tm20 macaca mula
112	213.5	27.2	203	2	Q4L212_AOTNA	Q4l212 aotus nancy
113	213	27.1	255	2	Q9I8I0_SALFO	Q9i8i0 salvelinus
114	212	27.0	127	2	Q9ERC9_MESAU	Q9erc9 mesocricetu
115	211	26.8	252	2	Q8K3Y7_RAT	Q8k3y7 rattus norv
116	208	26.5	255	2	Q9DEP9_ONCMY	Q9dep9 oncorhynchu
117	207	26.3	188	2	Q5BMN0_SALSA	Q5bmn0 salmo salar
118	207	26.3	246	2	Q5BMN2_SALSA	Q5bmn2 salmo salar
119	203	25.8	234	2	Q6T9C7_BRARE	Q6t9c7 brachydanio
120	203	25.8	239	2	Q50L61_CHICK	Q50l61 gallus gall
121	202	25.7	183	2	Q5HYS4_HUMAN	Q5hys4 homo sapien
122	201.5	25.6	231	2	Q8AW02_CYPCA	Q8aw02 cyprinus ca
123	201.5	25.6	237	2	Q8AWC9_CYPCA	Q8awc9 cyprinus ca
124	201	25.6	207	2	Q58G74_CHICK	Q58g74 gallus gall
125	200.5	25.5	192	2	Q5VJK8_HUMAN	Q5vjk8 homo sapien
126	200.5	25.5	251	2	Q3SX69_HUMAN	Q3sx69 homo sapien
127	200.5	25.5	251	2	Q8NFE9_HUMAN	Q8nfe9 homo sapien
128	199.5	25.4	252	2	Q80YZ0_MOUSE	Q80yz0 mus musculu
129	199.5	25.4	252	2	Q8K3Y8_MOUSE	Q8k3y8 mus musculu
130	198	25.2	160	2	Q5I6M8_SALSA	Q5i6m8 salmo salar
131	195.5	24.9	230	2	Q8JG37_ICTPU	Q8jg37 ictalurus p
132	195	24.8	110	2	Q7ZZX5_PAGMA	Q7zzx5 pagrus majo
133	193	24.6	41	2	Q9XT69_CANFA	Q9xt69 canis famil
134	185	23.5	174	1	TNF15_HUMAN	O95150 homo sapien
135	185	23.5	174	2	Q5VWH1_HUMAN	Q5vwh1 homo sapien
136	181.5	23.1	242	2	Q4W898_BRARE	Q4w898 brachydanio
137	179.5	22.8	253	2	Q5CAQ0_CHICK	Q5caq0 gallus gall
138	177.5	22.6	240	1	TNF14_HUMAN	O43557 h tumor nec
139	177.5	22.6	240	2	Q6FHA1_HUMAN	Q6fha1 homo sapien
140	177	22.5	244	1	TNFC_HUMAN	Q06643 homo sapien
141	177	22.5	244	2	Q5STB2_HUMAN	Q5stb2 homo sapien
142	176.5	22.5	278	1	TNFL6_RAT	P36940 r tumor nec
143	176	22.4	280	1	TNFL6_MACFA	P63308 m tumor nec
144	176	22.4	280	1	TNFL6_MACMU	P63307 m tumor nec
145	176	22.4	280	1	TNFL6_MACNE	P63306 m tumor nec
146	175	22.3	244	1	TNFC_PANTR	Q862z7 pan troglod
147	174	22.1	112	2	Q6J0S0_PERLE	Q6j0s0 peromyscus
148	174	22.1	244	1	TNFC_MACMU	Q5tm22 macaca mula
149	174	22.1	280	1	TNFL6_CERTO	Q9bdn1 c tumor nec
150	169.5	21.6	279	1	TNFL6_MOUSE	P41047 m tumor nec
151	169.5	21.6	279	2	Q544E9_MOUSE	Q544e9 m 0 day neo
152	164.5	20.9	279	2	Q7TMV9_MOUSE	Q7tmv9 mus musculu
153	163	20.7	239	1	TNF14_MOUSE	Q9qyh9 mus musculu
154	163	20.7	281	1	TNFL6_HUMAN	P48023 h tumor nec
155	163	20.7	281	2	Q53ZZ1_HUMAN	Q53zz1 homo sapien
156	162.5	20.7	227	2	Q7T2Q3_CYPCA	Q7t2q3 cyprinus ca
157	161	20.5	310	1	TNFC_MARMO	Q9jm10 marmota mon
158	156.5	19.9	282	1	TNFL6_PIG	Q9bea8 s tumor nec
159	156.5	19.9	299	2	Q2TPW2_CTEID	Q2tpw2 ctenopharyn
160	156	19.8	306	2	Q6MG45_RAT	Q6mg45 rattus norv
161	154.5	19.7	302	2	Q7TSL5_PERMA	Q7tsl5 peromyscus
162	154	19.6	238	2	Q2I7F4_ONCMY	Q2i7f4 oncorhynchu
163	153	19.5	158	2	Q5SP42_HUMAN	Q5sp42 homo sapien
164	152.5	19.4	299	2	Q6DHG9_BRARE	Q6dhg9 brachydanio
165	150.5	19.1	154	2	Q8MJ19_MACMU	Q8mj19 macaca mula
166	150.5	19.1	250	1	TNFC_MACEU	Q9xt47 macropus eu
167	150.5	19.1	280	1	TNFL6_FELCA	Q861w5 f tumor nec
168	150	19.1	306	1	TNFC_MOUSE	P41155 mus musculu
169	148.5	18.9	250	2	Q3T4H6_MACEU	Q3t4h6 macropus eu
170	146.5	18.6	150	1	TNFC_PIG	Q9tsv8 sus scrofa
171	143	18.2	131	2	Q6J3Q6_CANFA	Q6j3q6 canis famil
172	142	18.1	214	2	Q9DDZ5_BRARE	Q9ddz5 brachydanio
173	142	18.1	287	2	Q90WT9_CHICK	Q90wt9 gallus gall
174	142	18.1	317	2	Q7ZYX9_BRARE	Q7zyx9 brachydanio
175	140.5	17.9	234	2	Q50D53_GASAC	Q50d53 gasterosteu
176	140	17.8	169	2	Q9WV90_MARMO	Q9wv90 marmota mon
177	135	17.2	260	1	CD40L_RAT	Q9z2v2 rattus norv
178	132.5	16.9	287	2	Q8K3G0_RAT	Q8k3g0 rattus norv
179	131.5	16.7	260	1	CD40L_MOUSE	P27548 mus musculu
180	130.5	16.6	219	2	Q5EAP6_BRARE	Q5eap6 brachydanio
181	128.5	16.3	291	1	TNF10_MOUSE	P50592 mus musculu
182	128.5	16.3	291	2	Q3TZR6_MOUSE	Q3tzr6 mus musculu
183	128.5	16.3	291	2	Q3U5H0_MOUSE	Q3u5h0 mus musculu
184	128.5	16.3	303	2	Q5XKN3_MOUSE	Q5xkn3 mus musculu
185	128	16.3	318	1	TNF11_RAT	Q9ese2 r tumor nec
186	127	16.2	261	2	Q4TVR2_SHEEP	Q4tvr2 ovis aries
187	127	16.2	292	2	Q5ZK93_CHICK	Q5zk93 gallus gall
188	127	16.2	316	1	TNF11_MOUSE	O35235 m tumor nec
189	127	16.2	316	2	Q3TWY5_MOUSE	Q3twy5 mus musculu
190	126.5	16.1	304	2	Q7T1F2_CHICK	Q7t1f2 gallus gall
191	126	16.0	244	2	Q54A98_HUMAN	Q54a98 homo sapien
192	126	16.0	317	1	TNF11_HUMAN	O14788 h tumor nec
193	126	16.0	317	2	Q5T9Y4_HUMAN	Q5t9y4 homo sapien
194	124	15.8	261	1	CD40L_PIG	Q95mq5 sus scrofa
195	123	15.6	109	2	Q45NE6_HUMAN	Q45ne6 homo sapien
196	123	15.6	260	1	CD40L_CANFA	O97626 canis famil
197	123	15.6	260	1	CD40L_FELCA	O97605 felis silve
198	122.5	15.6	291	2	Q2I7F6_ONCMY	Q2i7f6 oncorhynchu
199	121.5	15.5	285	2	Q4SKU4_TETNG	Q4sku4 tetraodon n
200	121	15.4	88	2	Q90WP9_PLEPL	Q90wp9 pleuronecte

ALIGNMENTS

RESULT 1
TNFA_HUMAN
ID TNFA_HUMAN STANDARD; PRT; 233 AA.
AC P01375; O43647; Q9P1Q2; Q9UIV3;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 21-FEB-2006, entry version 85.
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN Name=TNF; Synonyms=TNFA, TNFSF2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87217060; PubMed=3555974;
RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
RA Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
RA Filippov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,
RA Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;
RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-
RT alpha) and lymphotoxin (TNF-beta) in the human genome.";
RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85086244; PubMed=6392892;
RA Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,
RA Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;
RT "Human tumour necrosis factor: precursor structure, expression and
RT homology to lymphotoxin.";
RL Nature 312:724-729(1984).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85137898; PubMed=3883195;
RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;
RT "Cloning and expression in Escherichia coli of the gene for human
RT tumour necrosis factor.";
RL Nature 313:803-806(1985).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86016093; PubMed=2995927;
RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,

RA Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;
RT "Human lymphotoxin and tumor necrosis factor genes: structure,
RT homology and chromosomal localization.";
RL Nucleic Acids Res. 13:6361-6373(1985).
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85142190; PubMed=3856324;
RA Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,
RA van Arsdell J.N., Yamamoto R., Mark D.F.;
RT "Molecular cloning of the complementary DNA for human tumor necrosis
RT factor.";
RL Science 228:149-154(1985).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86030296; PubMed=3932069;
RA Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
RA Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,
RA Ruysschaert M.R., van Vliet A., Fiers W.;
RT "Molecular cloning and expression of human tumor necrosis factor and
RT comparison with mouse tumor necrosis factor.";
RL Eur. J. Biochem. 152:515-522(1985).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93272029; PubMed=8499947;
RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
RA Cohen D.;
RT "Dense Alu clustering and a potential new member of the NF kappa B
RT family within a 90 kilobase HLA class III segment.";
RL Nat. Genet. 3:137-145(1993).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99218514; PubMed=10202016;
RA Neville M.J., Campbell R.D.;
RT "A new member of the Ig superfamily and a V-ATPase G subunit are among
RT the predicted products of novel genes close to the TNF locus in the
RT human MHC.";
RL J. Immunol. 162:4745-4754(1999).
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656967; DOI=10.1101/gr.1736803;
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA Campbell R.D., Hood L.;
RT "Analysis of the gene-dense major histocompatibility complex class III
RT region and its comparison to mouse.";
RL Genome Res. 13:2621-2636(2003).
RN [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Shiina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN [11]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
RT "Genome diversity in HLA: a new strategy for detection of genetic
RT polymorphisms in expressed genes within the HLA class III and class I
RT regions.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN [12]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN [13]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LEU-84.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN [14]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [15]
RP NUCLEOTIDE SEQUENCE OF 77-233.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN [16]
RP NUCLEOTIDE SEQUENCE OF 84-214.
RC TISSUE=Prostatic carcinoma;
RA Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [17]
RP PHOSPHORYLATION (MEMBRANE FORM).
RX MEDLINE=96170872; PubMed=8597870;
RA Pocsik E., Duda E., Wallach D.;
RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
RT transfected HeLa cells.";
RL J. Inflamm. 45:152-160(1995).
RN [18]
RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
RX MEDLINE=99221647; PubMed=10205166; DOI=10.1093/emboj/18.8.2119;
RA Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
RA Roufogalis B.D., Chaudhri G.;
RT "A casein kinase I motif present in the cytoplasmic domain of members
RT of the tumour necrosis factor ligand family is implicated in 'reverse
RT signalling'.";
RL EMBO J. 18:2119-2126(1999).
RN [19]
RP MUTAGENESIS.
RX MEDLINE=91184128; PubMed=2009860;
RA Ostade X.V., Tavernier J., Prange T., Fiers W.;
RT "Localization of the active site of human tumour necrosis factor
RT (hTNF) by mutational analysis.";
RL EMBO J. 10:827-836(1991).
RN [20]
RP MYRISTOYLATION.
RX MEDLINE=93018820; PubMed=1402651; DOI=10.1084/jem.176.4.1053;
RA Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;
RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
RT specific lysine residues.";
RL J. Exp. Med. 176:1053-1062(1992).
RN [21]
RP CLEAVAGE BY ADAM17.
RX MEDLINE=97186575; PubMed=9034191; DOI=10.1038/385733a0;
RA Moss M.L., Jin S.-L.C., Milla M.E., Burkhart W., Carter H.L.,
RA Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,
RA Mitchell J., Moyer M., Pahel G., Rocque W., Overton L.K., Schoenen F.,
RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
RT "Cloning of a disintegrin metalloproteinase that processes precursor
RT tumour-necrosis factor-alpha.";

```
RL   Nature 385:733-736(1997).
RN   [22]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=89159409; PubMed=2922050; DOI=10.1038/338225a0;
RA   Jones E.Y., Stuart D.I., Walker N.P.;
RT   "Structure of tumour necrosis factor.";
RL   Nature 338:225-228(1989).
RN   [23]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=91193276; PubMed=1964681;
RA   Jones E.Y., Stuart D.I., Walker N.P.;

  Query Match             100.0%;  Score 786;  DB 1;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 5e-67;
  Matches  151;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||||||||||||||||||:|||||||:|||||||||||||:||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 2
Q5STB3_HUMAN
ID   Q5STB3_HUMAN    PRELIMINARY;    PRT;   233 AA.
AC   Q5STB3;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-MAR-2006, entry version 8.
DE   Tumor necrosis factor (TNF superfamily, member 2).
GN   Name=TNF; ORFNames=DAQB-87N14.5-001, DASS-280D8.2-001,
GN   XXbac-BCX270M2.1-001, XXbac-BPG296P20.12-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood leukocyte;
RA   Shiina T., Ota M., Takasu M., Katsuyama Y., Hashimoto N., Tokunaga K.,
RA   Inoko H.;
RT   "Genome diversity in HLA: A new strategy for detection of genetic
RT   polymorphisms in expressed genes within the HLA class III and class I
RT   regions.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL662847; CAI17678.1; -; Genomic_DNA.
DR   EMBL; AL662801; CAI18292.1; -; Genomic_DNA.
DR   EMBL; AL929587; CAI18649.1; -; Genomic_DNA.
DR   EMBL; BX248519; CAI41940.1; -; Genomic_DNA.
DR   EMBL; AB202113; BAE78639.1; -; Genomic_DNA.
DR   SMR; Q5STB3; 82-233.
DR   Ensembl; ENSG00000111956; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   233 AA;  25644 MW;  3DF90F96C9031FFE CRC64;

  Query Match             100.0%;  Score 786;  DB 2;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 5e-67;
  Matches  151;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||||||||||||||||||:|||||||:|||||||||||||:||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233


RESULT 3
TNFA_PAPSP
ID   TNFA_PAPSP      STANDARD;       PRT;   233 AA.
AC   P33620;
DT   01-FEB-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 1.
DT   07-FEB-2006, entry version 40.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio sp. (Baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=61183;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Sanjanwala M., Edwards A.;
RL   Submitted (SEP-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X62141; CAA44068.1; -; Genomic_DNA.
DR   PIR; S22052; S22052.
DR   HSSP; P01375; 1A8M.
DR   SMR; P33620; 82-233.
DR   InterPro; IPR006053; TNF_abc.
```

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DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034443.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034444.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25557 MW;  455360B48DC74173 CRC64;

  Query Match             99.1%;  Score 779;  DB 1;  Length 233;
  Best Local Similarity   95.5%;  Pred. No. 2.3e-66;
  Matches  150;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||||||||||||||||:||||||:||||||||||||:||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| ||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 4
TNFA_PANTR
ID   TNFA_PANTR     STANDARD;      PRT;   232 AA.
AC   Q8HZD9;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 2.
DT   07-FEB-2006, entry version 30.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=22381002; PubMed=12493009;
RX   DOI=10.1034/j.1600-065X.2002.19008.x;
RA   Kulski J.K., Shiina T., Anzai T., Kohara S., Inoko H.;
RT   "Comparative genomic analysis of the MHC: the evolution of class I
RT   duplication blocks, diversity and complexity from shark to man.";
RL   Immunol. Rev. 190:95-122(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;
RA   Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA   Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA   Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA   Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT   "Comparative sequencing of human and chimpanzee MHC class I regions
RT   unveils insertions/deletions as the major path to genomic
RT   divergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 33-186.
RA   O'Huigin C., Tichy H., Klein J.;
RT   "Molecular evolution in higher primates; gene specific and organism
RT   specific characteristics.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB054536; BAB83882.1; -; Genomic_DNA.
DR   EMBL; BA000041; BAC78157.1; -; Genomic_DNA.
DR   EMBL; AY091964; AAM76582.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8HZD9; 81-232.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    232       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT                                /FTId=PRO_0000034437.
FT   CHAIN        77    232       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034438.
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     58    232       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    144    176       By similarity.
FT   CONFLICT     77     77       G -> VR (in Ref. 3).
SQ   SEQUENCE   232 AA;  25446 MW;  E4D71B19C6AE0D03 CRC64;

  Query Match             98.9%;  Score 777;  DB 1;  Length 232;
  Best Local Similarity   96.1%;  Pred. No. 3.6e-66;
  Matches  149;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 62
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 SSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 137
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Qy          63 LFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGG 122
               ||:||||||||||||||||||||||||||:|||||||:||||||||||||:||||||||||
Db         138 LFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGG 197

Qy         123 VFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               |||||:|||||||||||||||||||||||||||||
Db         198 VFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 232


RESULT 5
TNFA_MACMU
ID   TNFA_MACMU     STANDARD;      PRT;   233 AA.
AC   P48094; Q5TM21; Q8HZD6;
DT   01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1996, sequence version 1.
DT   07-FEB-2006, entry version 37.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15269276; DOI=10.1093/molbev/msh216;
RA   Kulski J.K., Anzai T., Shiina T., Inoko H.;
RT   "Rhesus macaque class I duplicon structures, organization, and
RT   evolution within the alpha block of the major histocompatibility
RT   complex.";
RL   Mol. Biol. Evol. 21:2079-2091(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 33-187.
RA   O'Huigin C., Tichy H., Klein J.;
RT   "Molecular evolution in higher primates; gene specific and organism
RT   specific characteristics.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U19850; AAA86712.1; -; mRNA.
DR   EMBL; AB128049; BAD69724.1; -; Genomic_DNA.
DR   EMBL; AY091967; AAM76585.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P48094; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034431.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034432.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25630 MW;  9F6F85050595FD59 CRC64;

  Query Match             97.7%;  Score 768;  DB 1;  Length 233;
  Best Local Similarity   94.3%;  Pred. No. 2.7e-65;
  Matches  148;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
               ||||||||||:|||||||||||||||||||||||||||||| ||||||||||||||||
Db          77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELTDNQLVVPSEGLYLIYS 136

Qy          61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
               ||||:||||| ||||||||||||||||:|||||:|||||||||||||:||||||||
Db         137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy         121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               |||||||:||||||||| ||||||||||||||||||
Db         197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 6
TNFA_MACFA
ID   TNFA_MACFA     STANDARD;      PRT;   233 AA.
AC   P79337;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1997, sequence version 1.
DT   07-FEB-2006, entry version 36.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lymphocyte;
RA   Tatsumi M.;
RT   "Molecular cloning and expression of cynomolgus monkey TNF-alpha.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
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CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB000513; BAA19131.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P79337; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034429.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034430.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25558 MW;  6ABF2C3AB132C217 CRC64;

  Query Match             97.3%;  Score 765;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 5.2e-65;
  Matches  147;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||:||||||||||||||||||||||:|||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALVANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||| ||||||||||||||||:|||||||:||||||||||||:||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| ||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 7
TNFA_PAPHU
ID   TNFA_PAPHU     STANDARD;      PRT;   233 AA.
AC   O77510;
DT   15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1998, sequence version 1.
DT   07-FEB-2006, entry version 35.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio hamadryas ursinus (Chacma baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=36229;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=98147379; PubMed=9488055; DOI=10.1016/S0161-5890(97)00124-7;
RA   Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT   "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RT   alpha.";
RL   Mol. Immunol. 34:1041-1042(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AF019963; AAC31675.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O77510; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034441.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034442.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25658 MW;  B9403255058D4A03 CRC64;

  Query Match             97.2%;  Score 764;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 6.5e-65;
  Matches  147;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||:|| |||||||||||||||||||||||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVVHVVANPQAEGQLQWLNRRANALLANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||| ||||||||||||||||:|||||||:||||||||||||:||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| ||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233
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RESULT 8
TNFA_PAPAN
ID   TNFA_PAPAN     STANDARD;      PRT;   233 AA.
AC   P59695;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 1.
DT   07-FEB-2006, entry version 27.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA   Villinger F.J., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY234222; AAO85335.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P59695; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT                                /FTId=PRO_0000034439.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034440.
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     58    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25736 MW;  0C477F9EB6CC9909 CRC64;

  Query Match             96.8%;  Score 761;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 1.3e-64;
  Matches  147;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||:||||||||||||||||||||||||||||  ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVEPTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||||:|||||| ||||||||||||||||:|||||||:||||||||||||:||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||| ||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 9
O97543_AOTNA
ID   O97543_AOTNA   PRELIMINARY;   PRT;   149 AA.
AC   O97543;
DT   01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1999, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF014513; AAD01539.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O97543; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16466 MW;  3C2A6140778EFA8A CRC64;

  Query Match             95.5%;  Score 751;  DB 2;  Length 149;
  Best Local Similarity   96.0%;  Pred. No. 6.4e-64;
  Matches  143;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ 60

Qy         68 GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
              ||||||||||||||||||||:|||||||:|||||||||||||:|||||||||||||||
Db         61 GCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLE 120

Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIA 156
              :|||||||||||||||||||||||||||
Db        121 KGDRLSAEINRPDYLDFAESGQVYFGIIA 149


RESULT 10
TNFA_CANFA
ID   TNFA_CANFA     STANDARD;      PRT;   233 AA.
AC   P51742; Q28339;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-FEB-2006, entry version 39.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Fiers W.;
RT   "Tumour necrosis factor.";
RL   (In) Sim E. (eds.);
RL   The natural immune system humoral factors, pp.65-119, IRL Press,
RL   Oxford (1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT   "Cloning and expression of the cDNA for canine tumor necrosis factor-
RT   alpha in E. coli.";
RL   Lymphokine Res. 13:191-196(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Wagner J.L., Palti Y., DiDario D.D.;
RT   "Genomic map of a portion of the canine MHC class I histocompatibility
RT   complex.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 74-205.
RC   STRAIN=Beagle; TISSUE=Blood;
RA   Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RT   "Expression of canine TNF, IL-1 and IL-6 mRNAs in peripheral blood
RT   monocytes and cell lines.";
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X94932; CAA64403.1; -; Genomic_DNA.
DR   EMBL; S74068; AAB32391.1; -; mRNA.
DR   EMBL; AY423389; AAR27885.1; -; Genomic_DNA.
DR   EMBL; Z70046; CAA93908.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P51742; 82-233.
DR   Ensembl; ENSCAFG00000000517; Canis familiaris.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034409.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034410.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2    *  Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
FT   CONFLICT     59     60       QR -> PE (in Ref. 2).
FT   CONFLICT     66     66       G -> C (in Ref. 2).
FT   CONFLICT     74     74       A -> V (in Ref. 4).
FT   CONFLICT    111    111       A -> D (in Ref. 2).
FT   CONFLICT    116    116       G -> D (in Ref. 2).
FT   CONFLICT    134    135       IY -> DS (in Ref. 2).
SQ   SEQUENCE   233 AA;  25447 MW;  7B2588FBC8B25340 CRC64;

  Query Match             94.8%;  Score 745;  DB 1;  Length 233;
  Best Local Similarity   89.8%;  Pred. No. 4.4e-63;
  Matches  141;  Conservative   12;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |:||||||||:||||||||:||||||||:||||||||||||| ||||:|||:|||||||
Db         77 VKSSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLIVPSDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||||||||||||| ||||||:|||||||:|||||||||| ||:|||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQRETPEGTEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:||||||||| |:||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPNYLDFAESGQVYFGIIAL 233


RESULT 11
Q2MJ87_TRIMA
ID   Q2MJ87_TRIMA   PRELIMINARY;   PRT;   233 AA.
AC   Q2MJ87;
DT   07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   07-FEB-2006, sequence version 1.
DT   07-FEB-2006, entry version 1.
DE   Tumor necrosis factor alpha.
OS   Trichechus manatus latirostris.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Afrotheria; Sirenia; Trichechidae; Trichechus.
OX   NCBI_TaxID=127582;
RN   [1]
```

```
RP   NUCLEOTIDE SEQUENCE.
RA   Colle C.F. III, Walsh C.J.;
RT   "Molecular cloning and functional characterization of the Florida
RT   manatee (Trichechus manatus) tumor necrosis facter alpha.";
RL   Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; DQ333395; ABC58216.1; -; mRNA.
SQ   SEQUENCE   233 AA;  25625 MW;  475200AA9BC34665 CRC64;

  Query Match             94.0%;  Score 739;  DB 2;  Length 233;
  Best Local Similarity   90.4%;  Pred. No. 1.7e-62;
  Matches  142;  Conservative   11;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||:||||||||||||||||:|||||||||||| ||||:|||:|||||||
Db         77 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSRRANALLANGVELIDNQLMVPSDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||||||||||||||||:|||||||:||| ||||| |||:||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCHRETPEEAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:||||||||  |:||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPNYLDFAESGQVYFGIIAL 233


RESULT 12
TNFA_FELCA
ID   TNFA_FELCA     STANDARD;      PRT;   233 AA.
AC   P19101; Q8HYM0;
DT   01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 2.
DT   07-FEB-2006, entry version 46.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   MEDLINE=91016860; PubMed=2216740;
RA   McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
RT   "Gene sequence of feline tumor necrosis factor alpha.";
RL   Nucleic Acids Res. 18:5563-5563(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Bone marrow;
RA   Daniel S.L., Brenner C.A., Legendre A.M., Soloman A., Rouse B.T.;
RT   "Feline cytokines TNF alpha and IL-1 beta: PCR cloning and sequencing
RT   of cDNA.";
RL   Anim. Biotechnol. 3:117-121(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 95-185.
RA   Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;
RT   "Characterization of 8 feline type I markers.";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; X54000; CAA37948.1; -; Genomic_DNA.
DR   EMBL; M92061; AAA30818.1; -; mRNA.
DR   EMBL; AF459810; AAO15590.1; -; Genomic_DNA.
DR   PIR; S11688; S11688.
DR   HSSP; P01375; 4TSV.
DR   SMR; P19101; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034419.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034420.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
FT   CONFLICT     28     28       G -> R (in Ref. 2).
FT   CONFLICT    104    104       W -> R (in Ref. 1).
FT   CONFLICT    141    141       T -> K (in Ref. 3).
FT   CONFLICT    151    151       L -> H (in Ref. 2).
FT   CONFLICT    155    155       T -> A (in Ref. 1).
FT   CONFLICT    210    210       T -> A (in Ref. 2).
SQ   SEQUENCE   233 AA;  25382 MW;  03E51823A7863510 CRC64;

  Query Match             93.8%;  Score 737;  DB 1;  Length 233;
  Best Local Similarity   89.8%;  Pred. No. 2.6e-62;
  Matches  141;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||:|||||||||:||||||||:|||||||||||| |||| |||:|||||||
Db         77 LRSSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLKVPSDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||||||||||| ||||||:|||||||:||||||||||||:||||||||
Db        137 QVLFTGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||  ||| | ||||||||||||||||
Db        197 GGVFQLEKGDRLSTEINLPAYLDFAESGQVYFGIIAL 233


RESULT 13
Q2LAH3_DICBI
ID   Q2LAH3_DICBI   PRELIMINARY;   PRT;   233 AA.
AC   Q2LAH3;
DT   21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   21-FEB-2006, sequence version 1.
```

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DT   21-FEB-2006, entry version 1.
DE   Tumor necrosis factor alpha.
OS   Diceros bicornis (Black rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Rhinocerotidae;
OC   Diceros.
OX   NCBI_TaxID=9805;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Colle C.F. III, Walsh C.J.;
RT   "Molecular cloning and functional characterization of the black
RT   rhinoceros (Diceros bicornis) tumor necrosis factor alpha.";
RL   Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; DQ340435; ABC68489.1; -; mRNA.
SQ   SEQUENCE   233 AA;  25460 MW;  C42BD327A3804BC1 CRC64;

  Query Match             91.9%;  Score 722;  DB 2;  Length 233;
  Best Local Similarity   88.5%;  Pred. No. 7.2e-61;
  Matches  139;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||| |||:||||||||||||||||||: |||||||||||| ||||||| :|||||||
Db         77 LRSSSRNPSDKPVAHVVANPQAEGQLQWLSGRANALLANGVELTDNQLVVPVDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||| |||||||||||| |||||||:|||||||:|||| ||||||||:||||||||
Db        137 QVLFRGQGCSSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQTETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||:||:||||||||| ||||||||||||||||||||
Db        197 GGVFKLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 14
TNFA_SAISC
ID   TNFA_SAISC     STANDARD;      PRT;   233 AA.
AC   Q8MKG8;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
RA   Heraud J.M., Lavergne A., Kazanji M.;
RT   "Molecular cloning, characterization, and quantification of squirrel
RT   monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL   Immunogenetics 54:20-29(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22516846; PubMed=12628762; DOI=10.1016/S0165-2427(03)00018-7;
RA   Merien F., Lavergne A., Behr C., Contamin H.;
RT   "Sequencing and analysis of genomic DNA and cDNA encoding TNF-alpha in
RT   the squirrel monkey (Saimiri sciureus).";
RL   Vet. Immunol. Immunopathol. 92:37-43(2003).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF294760; AAK92047.1; -; mRNA.
DR   EMBL; AJ437697; CAD27179.1; -; Genomic_DNA.
DR   EMBL; AJ437698; CAD27180.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8MKG8; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT                                /FTId=PRO_0000034453.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034454.
FT   TOPO_DOM      1     32       Cytoplasmic (Potential).
FT   TRANSMEM     33     55       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     56    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25578 MW;  197FB066F744FCAD CRC64;

  Query Match             90.8%;  Score 714;  DB 1;  Length 233;
  Best Local Similarity   87.3%;  Pred. No. 4.2e-60;
  Matches  137;  Conservative   11;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||| |||:||||||||||||||||||||||||||||||||||||:||||:||
Db         77 VRSSSRIPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSDGLYLVYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||||  ||||:||||||||| :|||||||:|||||||| ||: :||||||||
Db        137 QVLFKGQGCPSTFTLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTHPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||: || || ||||||||||||
Db        197 GGVFQLEKGDRLSAEISPPDSLDLAESGQVYFGIIAL 233


RESULT 15
TNFA_HORSE
ID   TNFA_HORSE     STANDARD;      PRT;   234 AA.
AC   P29553; Q9TTJ3;
DT   01-APR-1993, integrated into UniProtKB/Swiss-Prot.
DT   01-APR-1993, sequence version 1.
DT   07-FEB-2006, entry version 41.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
```

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DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92084125; PubMed=1748301; DOI=10.1016/0378-1119(91)90333-7;
RA   Su X., Morris D.D., McGraw R.A.;
RT   "Cloning and characterization of gene TNF alpha encoding equine tumor
RT   necrosis factor alpha.";
RL   Gene 107:319-321(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Thoroughbred; TISSUE=Artery;
RA   Ishida N., Sato F., Hasegawa T.;
RT   "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M64087; AAA30959.1; -; Genomic_DNA.
DR   EMBL; AB035735; BAA88349.1; -; mRNA.
DR   PIR; JQ1344; JQ1344.
DR   HSSP; P01375; 1A8M.
DR   SMR; P29553; 83-234.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    234       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034421.
FT   CHAIN        78    234       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034422.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    234       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    146    178       By similarity.
FT   CONFLICT    177    179       PCH -> LAN (in Ref. 2).
SQ   SEQUENCE   234 AA;  25469 MW;  E79ACE91143DF373 CRC64;
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  Query Match           89.6%;  Score 704;  DB 1;  Length 234;
  Best Local Similarity   85.4%;  Pred. No. 3.9e-59;
  Matches  134;  Conservative   16;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||:|||||||||||||||||: ||||||||||:| ||||||| :|||||||
Db         78 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSGRANALLANGVKLTDNQLVVPLDGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||||||||||||:|||| ::|||||||:|||  |:|| |||:||||||||
Db        138 QVLFKGQGCPSTHVLLTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPWYEPIYL 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:||:||||||:|:|||||||||||||||||
Db        198 GGVFQLEKGDQLSAEINQPNYLDFAESGQVYFGIIAL 234


RESULT 16
O97538_AOTVO
ID   O97538_AOTVO   PRELIMINARY;   PRT;   149 AA.
AC   O97538;
DT   01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1999, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus vociferans (Spix's owl monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=57176;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF014508; AAD01534.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O97538; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16415 MW;  86F1B9BCED16E689 CRC64;

  Query Match           89.4%;  Score 703;  DB 2;  Length 149;
  Best Local Similarity   89.3%;  Pred. No. 2.7e-59;
  Matches  133;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              |||:||||||||||||||||||||||||||||||||||||||||||:||||||:||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLVYSQVLFKGQ 60
```

```
Qy          68 GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
               ||||| :||||:|||||||||| :|||||||:|||||||| ||: :|||||||||||||||
Db          61 GCPSTFMLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTNPWYEPIYLGGVFQLE 120

Qy         128 XGDRLSAEINRPDYLDFAESGQVYFGIIA 156
               :||||||||| ||||| ||||||||||||
Db         121 KGDRLSAEINLPDYLDLAESGQVYFGIIA 149


RESULT 17
Q9TTG8_AOTNI
ID   Q9TTG8_AOTNI   PRELIMINARY;   PRT;  149 AA.
AC   Q9TTG8;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus nigriceps (Black-headed owl monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=57175;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF097328; AAF21303.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9TTG8; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16415 MW;  86F1B9BCED16E689 CRC64;

  Query Match             89.4%;  Score 703;  DB 2;  Length 149;
  Best Local Similarity   89.3%;  Pred. No. 2.7e-59;
  Matches  133;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy           8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
               |||:||||||||||||||||||||||||||||||||||||||||||:||||||:||
Db           1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLVYSQVLFKGQ 60

Qy          68 GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
               ||||| :||||:|||||||||| :|||||||:|||||||| ||: :|||||||||||||||
Db          61 GCPSTFMLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTNPWYEPIYLGGVFQLE 120

Qy         128 XGDRLSAEINRPDYLDFAESGQVYFGIIA 156
               :||||||||| ||||| ||||||||||||
Db         121 KGDRLSAEINLPDYLDLAESGQVYFGIIA 149


RESULT 18
Q9BEG0_CYCDI
ID   Q9BEG0_CYCDI   PRELIMINARY;   PRT;   217 AA.
AC   Q9BEG0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Cyclopes didactylus (Silky anteater).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Xenarthra; Myrmecophagidae; Cyclopes.
OX   NCBI_TaxID=84074;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286828; CAC28514.1; -; Genomic_DNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q9BEG0; 74-217.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     217    217
SQ   SEQUENCE   217 AA;  23753 MW;  F760E887F6C29EBB CRC64;

  Query Match             88.8%;  Score 698;  DB 2;  Length 217;
  Best Local Similarity   87.9%;  Pred. No. 1.3e-58;
  Matches  131;  Conservative   13;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
               :|||||||||:||||||||||||||||:|||||||||||||| ||||||||:|||||||
Db          69 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSRRANALLANGVELTDNQLVVPSDGLYLIYS 128

Qy          61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
               ||||:|||||| |||||||::| |||||:|||||||:|||||||||| ||:|||||||||
Db         129 QVLFKGQGCPSAHVLLTHTVNRFAVSYQTKVNLLSAIKSPCQRETPEGPEAKPWYEPIYL 188

Qy         121 GGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
               |||||::|||||||||| |:|||||||||
Db         189 GGVFQLDKGDRLSAEINLPEYLDFAESGQ 217


RESULT 19
Q9BEG1_BRATR
ID   Q9BEG1_BRATR   PRELIMINARY;   PRT;   217 AA.
AC   Q9BEG1;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
```

```
GN   Name=tnfa;
OS   Bradypus tridactylus (Pale-throated three-toed sloth).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Xenarthra; Bradypodidae; Bradypus.
OX   NCBI_TaxID=9354;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286827; CAC28513.1; -; Genomic_DNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q9BEG1; 74-217.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     217    217
SQ   SEQUENCE   217 AA;  23655 MW;  A7056710B6238074 CRC64;

  Query Match             88.3%;  Score 694;  DB 2;  Length 217;
  Best Local Similarity   87.9%;  Pred. No. 3.2e-58;
  Matches  131;  Conservative   12;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||:||||||||||||||||:|||||||||||| ||||||||:|||||||
Db         69 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSRRANALLANGVELTDNQLVVPSDGLYLIYS 128

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||| |||||||::| |||||||:|||||||:|||||||||| | :||||||||
Db        129 QVLFKGQGCPSTPVLLTHTVNRFAVSYQTKVNLLSAIKSPCQRETPEGTEGKPWYEPIYL 188

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              ||||||::||||||||| ||||||||||
Db        189 GGVFQLDKGDRLSAEINLPDYLDFAESGQ 217


RESULT 20
TNFA_DELLE
ID   TNFA_DELLE     STANDARD;      PRT;   233 AA.
AC   Q8WNR1;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-MAR-2002, sequence version 1.
DT   07-FEB-2006, entry version 29.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Delphinapterus leucas (Beluga whale).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC   Odontoceti; Monodontidae; Delphinapterus.
OX   NCBI_TaxID=9749;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=21618234; PubMed=11768130;
RA   Denis F., Archambault D.;
RT   "Molecular cloning and characterization of beluga whale
RT   (Delphinapterus leucas) interleukin-1beta and tumor necrosis factor-
RT   alpha.";
RL   Can. J. Vet. Res. 65:233-240(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF320323; AAL56946.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8WNR1; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Phosphorylation; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034417.
FT   CHAIN        78    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034418.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   CARBOHYD     95     95       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25420 MW;  2DF37DCB2BC9E961 CRC64;

  Query Match             87.4%;  Score 687;  DB 1;  Length 233;
  Best Local Similarity   83.4%;  Pred. No. 1.7e-57;
  Matches  131;  Conservative   15;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:| |::|||||||  |:|||:||| || |||| |:| |||||||::|||||||
Db         77 LRSSSKTSSNKPVAHVVANLSAQGQLRWLNTYANTLLANSVKLEDNQLVVPTDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||||: |||||||||||||:|||||||:|||||||||||||:|||||||
Db        137 QVLFRGQGCPSTHLFLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYQ 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||| ||||||||||||||||||
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Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 21
TNFA_PIG
ID   TNFA_PIG       STANDARD;      PRT;   232 AA.
AC   P23563;
DT   01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1991, sequence version 1.
DT   07-FEB-2006, entry version 45.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=91016861; PubMed=2216741;
RA   Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;
RT   "Gene sequence of porcine tumor necrosis factor alpha.";
RL   Nucleic Acids Res. 18:5564-5564(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   TISSUE=Liver;
RX   MEDLINE=91340150; PubMed=1874444; DOI=10.1016/0378-1119(91)90075-M;
RA   Kuhnert P., Wuethrich C., Peterhans E., Pauli U.;
RT   "The porcine tumor necrosis factor-encoding genes: sequence and
RT   comparative analysis.";
RL   Gene 102:171-178(1991).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Macrophage;
RA   Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;
RT   "Complete nucleotide sequence of a cDNA encoding porcine tumor
RT   necrosis factor-alpha.";
RL   Anim. Biotechnol. 2:97-105(1991).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Large white; TISSUE=Fibroblast;
RX   MEDLINE=21108615; PubMed=11169259;
RX   DOI=10.1034/j.1399-0039.2001.057001055.x;
RA   Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
RA   Renard C.;
RT   "Sequence of the swine major histocompatibility complex region
RT   containing all non-classical class I genes.";
RL   Tissue Antigens 57:55-65(2001).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 44-232.
RX   MEDLINE=90034181; PubMed=2478420; DOI=10.1016/0378-1119(89)90350-8;
RA   Pauli U., Beutler B., Peterhans E.;
RT   "Porcine tumor necrosis factor alpha: cloning with the polymerase
RT   chain reaction and determination of the nucleotide sequence.";
RL   Gene 81:185-191(1989).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X54001; CAA37949.1; -; Genomic_DNA.
DR   EMBL; X54859; CAA38639.1; -; Genomic_DNA.
DR   EMBL; X57321; CAA40591.1; -; mRNA.
DR   EMBL; AJ251914; CAB63852.1; -; Genomic_DNA.
DR   EMBL; M29079; AAA31128.1; -; mRNA.
DR   PIR; S12606; S12606.
DR   HSSP; P01375; 4TSV.
DR   SMR; P23563; 84-232.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN          1    232       Tumor necrosis factor, membrane form.
FT                                 /FTId=PRO_0000034445.
FT   CHAIN         77    232       Tumor necrosis factor, soluble form.
FT                                 /FTId=PRO_0000034446.
FT   TOPO_DOM       1     35       Cytoplasmic (Potential).
FT   TRANSMEM      36     56       Signal-anchor for type II membrane
FT                                 protein (Potential).
FT   TOPO_DOM      57    232       Extracellular (Potential).
FT   SITE          76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES        2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID     144    176       By similarity.
SQ   SEQUENCE   232 AA;  25254 MW;  65B28F702D99C8BE CRC64;

  Query Match             87.2%;  Score 685.5;  DB 1;  Length 232;
  Best Local Similarity   85.4%;  Pred. No. 2.3e-57;
  Matches  134;  Conservative   15;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:| ||:|||||||| :||||||| :  |||||||||:|:||||||::|||||||
Db         77 LRSSSQT-SDKPVAHVVANVKAEGQLQWQSGYANALLANGVKLKDNQLVVPTDGLYLIYS 135

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||||:| |||||||||||||:|||||||:|||||||||||||:|||||||||
Db        136 QVLFRGQGCPSTNVFLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 195

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||: |||||||| ||||||||||||||||||||
Db        196 GGVFQLEKDDRLSAEINLPDYLDFAESGQVYFGIIAL 232


RESULT 22
Q2LAH2_STEBR
ID   Q2LAH2_STEBR   PRELIMINARY;   PRT;   233 AA.
AC   Q2LAH2;
DT   21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   21-FEB-2006, sequence version 1.
DT   21-FEB-2006, entry version 1.
DE   Tumor necrosis factor alpha.
OS   Steno bredanensis (Rough-toothed dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC   Odontoceti; Delphinidae; Steno.
OX   NCBI_TaxID=46167;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Colle C.F. III, Walsh C.J.;
RT   "Molecular cloning and functional characterization of the rough-
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RT   toothed dolphin (Steno bredanensis) tumor necrosis factor alpha.";
RL   Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; DQ340436; ABC68490.1; -; mRNA.
SQ   SEQUENCE   233 AA;  25419 MW;  6C1739CB2BD859DD CRC64;

  Query Match             86.1%;  Score 677;  DB 2;  Length 233;
  Best Local Similarity   82.2%;  Pred. No. 1.5e-56;
  Matches  129;  Conservative   15;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:| |::|||||||   :|||:||| || |||| |:| ||||||||::|||||||
Db         77 LRSSSKTSSNKPVAHVVANLSTQGQLRWLNTYANTLLANSVKLEDNQLVVPTDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||||: |||||||||||| |:|||||||:|||||||||||||:|||||||
Db        137 QVLFRGQGCPSTHLFLTHTISRIAVSYPTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYQ 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| ||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 23
TNFA_TURTR
ID   TNFA_TURTR     STANDARD;      PRT;   233 AA.
AC   Q9BEA1;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 32.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC   Odontoceti; Delphinidae; Tursiops.
OX   NCBI_TaxID=9739;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=21472839; PubMed=11587733; DOI=10.1016/S0165-2427(01)00353-1;
RA   Shoji Y., Inoue Y., Sugisawa H., Itou T., Endo T., Sakai T.;
RT   "Molecular cloning and functional characterization of bottlenose
RT   dolphin (Tursiops truncatus) tumor necrosis factor alpha.";
RL   Vet. Immunol. Immunopathol. 82:183-192(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB049358; BAB39855.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9BEA1; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Phosphorylation; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034459.
FT   CHAIN        78    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034460.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   CARBOHYD     95     95       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25404 MW;  71CC39C699CC49D9 CRC64;

  Query Match             85.1%;  Score 669;  DB 1;  Length 233;
  Best Local Similarity   80.9%;  Pred. No. 9e-56;
  Matches  127;  Conservative   17;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:| |::|||||||   :|||:||| || |||| |:| ||||||||::|||||||
Db         77 LRSSSKTSSNKPVAHVVANLSTQGQLRWLNTYANTLLANSVKLEDNQLVVPTDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||||: |||||||||||| ::|||||||:|||||||||||||:|||||||
Db        137 QVLFRGQGCPSTHLFLTHTISRIAVSYPSKVNLLSAIKSPCQRETPEGAEAKPWYEPIYQ 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| |||||||:||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAKSGQVYFGIIAL 233


RESULT 24
Q9BEF4_CABUN
ID   Q9BEF4_CABUN   PRELIMINARY;   PRT;   217 AA.
AC   Q9BEF4;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Cabassous unicinctus (Southern naked-tailed armadillo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Xenarthra; Dasypodidae; Cabassous.
OX   NCBI_TaxID=48852;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286829; CAC28518.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9BEF4; 74-217.
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DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     217    217
SQ   SEQUENCE   217 AA;  23742 MW;  83C591DD6883FD86 CRC64;

  Query Match             83.7%;  Score 658;  DB 2;  Length 217;
  Best Local Similarity   83.2%;  Pred. No. 9.4e-55;
  Matches  124;  Conservative   15;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:| :|:|||||||||||||| || |||| |||||:|| |||||||| |||||||
Db         69 LRSSSQTQNDKPVAHVVANPQAEGQLLWLGRRANTLLANGMELTDNQLVVPSGGLYLIYS 128

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|| |||||||||||:| : ||||:|||||||:|||||||||||:||||||||
Db        129 QVLFTGQSCPSTHVLLTHTINRFSASYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 188

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              ||||:|::||||||||| |:|||||||||
Db        189 GGVFRLDKGDRLSAEINLPEYLDFAESGQ 217


RESULT 25
Q9TTG7_AOTLE
ID   Q9TTG7_AOTLE   PRELIMINARY;   PRT;   138 AA.
AC   Q9TTG7;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 21.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus lemurinus (Northern gray-necked night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=43147;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF097329; AAF21304.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9TTG7; 1-137.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   138 AA;  15269 MW;  29275EE4F4CD5068 CRC64;

  Query Match             82.7%;  Score 650;  DB 2;  Length 138;
  Best Local Similarity   89.1%;  Pred. No. 3e-54;
  Matches  122;  Conservative   10;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              |||:||||||||||||||||||||||||||||||||||||||||||||:||||||:||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLVYSQVLFKGQ 60

Qy         68 GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
              ||||| :||||:||||||||| :|||||||:|||||||| ||: :|||||||||||||
Db         61 GCPSTFMLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTNPWYEPIYLGGVFQLE 120

Qy        128 XGDRLSAEINRPDYLDF 144
              :||||||||| ||||||
Db        121 KGDRLSAEINLPDYLDF 137


RESULT 26
TNFA_CAPHI
ID   TNFA_CAPHI     STANDARD;      PRT;   234 AA.
AC   P13296; Q28320; Q9MYZ2;
DT   01-JAN-1990, integrated into UniProtKB/Swiss-Prot.
DT   06-JUN-2002, sequence version 2.
DT   07-FEB-2006, entry version 55.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Splenocyte;
RA   Takakura H., Mori Y., Tatsumi M.;
RT   "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RT   E.coli and insect cells.";
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 41-234.
RA   Goldstein I.M., Henner D., Talhouk A.;
RL   Submitted (MAR-1989) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 44-234.
RC   TISSUE=Ovarian follicle;
RA   Wang B., Zhang Y.;
RT   "Goat ovarian TNF alpha cDNA sequence.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 75-234.
RC   TISSUE=Blood;
RA   Rimstad E.;
RL   Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
```

```
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   -!- CAUTION: Ref.2 sequence differs from that shown due to a
CC       frameshift in position 60.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D86587; BAA13130.1; -; mRNA.
DR   EMBL; X14828; CAA32937.1; ALT_FRAME; mRNA.
DR   EMBL; AF276985; AAF87741.1; -; mRNA.
DR   EMBL; X77317; CAA54523.1; -; mRNA.
DR   PIR; S06192; S06192.
DR   HSSP; P01375; 4TSV.
DR   SMR; P13296; 83-234.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Phosphorylation; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    234       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034411.
FT   CHAIN        79    234       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034412.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         78     79       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    146    178       By similarity.
FT   CONFLICT     79     79       R -> S (in Ref. 4).
FT   CONFLICT    119    119       E -> A (in Ref. 4).
FT   CONFLICT    129    129       T -> N (in Ref. 4).
FT   CONFLICT    155    155       H -> Q (in Ref. 4).
FT   CONFLICT    164    164       Y -> D (in Ref. 4).
FT   CONFLICT    184    184       E -> EG (in Ref. 4).
FT   CONFLICT    185    185       Missing (in Ref. 2).
FT   CONFLICT    215    215       Q -> L (in Ref. 3 and 4).
SQ   SEQUENCE   234 AA;  25519 MW;  9768E33BBBABB041 CRC64;

  Query Match             82.6%;  Score 649;  DB 1;  Length 234;
  Best Local Similarity   79.0%;  Pred. No. 7.7e-54;
  Matches  124;  Conservative   19;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||  | |||:| :  |||| ||||||:|||||||::|||||||
Db         78 LRSSSQASSNKPVAHVVANISAPGQLRWGDSYANALKANGVELKDNQLVVPTDGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:| ||||| : |||||||||||||:||:||||:||| |||||||||:|||||||
Db        138 QVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEGAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||:|:|||:|||||||||||||
Db        198 GGVFQLEKGDRLSAEINQPEYLDYAESGQVYFGIIAL 234
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RESULT 27
Q53ZM5_CAPHI
ID   Q53ZM5_CAPHI   PRELIMINARY;   PRT;   234 AA.
AC   Q53ZM5;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Tumor necrosis factor alpha.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Li C.H., Wei X.F., Xu L.X., Li X.R.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY304502; AAP68801.1; -; mRNA.
DR   SMR; Q53ZM5; 83-234.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   234 AA;  25504 MW;  9768E32E619BB041 CRC64;

  Query Match             82.2%;  Score 646;  DB 2;  Length 234;
  Best Local Similarity   79.0%;  Pred. No. 1.5e-53;
  Matches  124;  Conservative   18;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||  | |||:| :  |||| ||||||:|||||||::|||||||
Db         78 LRSSSQASSNKPVAHVVANISAPGQLRWGDSYANALKANGVELKDNQLVVPTDGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:| ||||| : |||||||||||||:||:||||:||| |||||||||:|||||||
Db        138 QVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEGAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||:|:|||:|||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPEYLDYAESGQVYFGIIAL 234


RESULT 28
TNFA_CAVPO
ID   TNFA_CAVPO     STANDARD;      PRT;   234 AA.
AC   P51435;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-FEB-2006, entry version 37.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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OC   Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Hartley; TISSUE=Lung;
RA   Yuan H.T., Kelly F.J., Bingle C.D.;
RT   "Cloning and characterisation of guinea pig TNF-alpha cDNA.";
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Dunkin-Hartley;
RX   MEDLINE=97462215; PubMed=9316485;
RA   White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT   "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT   factor-alpha.";
RL   Am. J. Physiol. 273:L524-L530(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U39839; AAB06492.1; -; mRNA.
DR   EMBL; U77036; AAB19210.1; -; mRNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; P51435; 87-234.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    234       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034413.
FT   CHAIN        80    234       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034414.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    234       Extracellular (Potential).
FT   SITE         79     80       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    147    178       By similarity.
SQ   SEQUENCE   234 AA;  25794 MW;  7272C940393E7E9B CRC64;

  Query Match             82.0%;  Score 644.5;  DB 1;  Length 234;
  Best Local Similarity   76.4%;  Pred. No. 2.1e-53;
  Matches  120;  Conservative   25;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||:|:  :|:|||||||| ||| :||||::||||||||: | ||||||||:|||||||

Db         79 LRSASQNDNDKPVAHVVANQQAEEELQWLSKRANALLANGMGLSDNQLVVPSDGLYLIYS 138

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||| ::|||||:||:|||| :|||||||:||||:|||||| :||||||||
Db        139 QVLFKGQGCPS-YLLLTHTVSRLAVSYPEKVNLLSAIKSPCQKETPEGAERKPWYEPIYL 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||::||||||:| | |||||:|||:|||
Db        198 GGVFQLQKGDRLSAEVNLPQYLDFADSGQIYFGVIAL 234


RESULT 29
Q9BEC4_TALEU
ID   Q9BEC4_TALEU   PRELIMINARY;   PRT;   216 AA.
AC   Q9BEC4;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Talpa europaea (European mole).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Insectivora; Talpidae; Talpa.
OX   NCBI_TaxID=9375;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286831; CAC28539.1; -; Genomic_DNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q9BEC4; 73-216.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     216    216
SQ   SEQUENCE   216 AA;  23542 MW;  FFFEFE8DBBD27836 CRC64;

  Query Match             81.7%;  Score 642;  DB 2;  Length 216;
  Best Local Similarity   82.6%;  Pred. No. 3.2e-53;
  Matches  123;  Conservative   14;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||||| |:|||||||||||||||:: |||||||||| :|||||||:|||||||
Db         68 LRSSSRTPGDKPVAHVVANPQAEGQLQWLSQVANALLANGVELTNNQLVVPSDGLYLIYS 127

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||  ||||| | | ||||: :|:|||||:||||||||||||:||||||||
Db        128 QVLFKGQGCPSNLVLLTHKIQRTAVSYEDAVDLLSAIKSPCQRETPEGAEARPWYEPIYL 187

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |||||||:|||||| || | |||||:|||
Db        188 GGVFQLEKGDRLSANINLPKYLDFAQSGQ 216
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RESULT 30
TNFA_MOUSE
ID   TNFA_MOUSE     STANDARD;      PRT;   235 AA.
AC   P06804; O35853; Q62326; Q91VF3;
DT   01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT   01-JUL-1989, sequence version 2.
DT   07-FEB-2006, entry version 69.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=Tnf; Synonyms=Tnfa, Tnfsf2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88224564; PubMed=2836146;
RA   Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;
RT   "Cloning and expression in Escherichia coli of the gene for mouse
RT   tumor necrosis factor.";
RL   DNA 7:193-201(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85298296; PubMed=3898078;
RA   Pennica D., Hayflick J.S., Bringman T.S., Palladino M.A.,
RA   Goeddel D.V.;
RT   "Cloning and expression in Escherichia coli of the cDNA for murine
RT   tumor necrosis factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86149365; PubMed=2419912;
RA   Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,
RA   Cerami A.;
RT   "Identification of a common nucleotide sequence in the 3'-untranslated
RT   region of mRNA molecules specifying inflammatory mediators.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85242112; PubMed=2989794;
RA   Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,
RA   Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,
RA   Ruysschaert M.-R., Fiers W.;
RT   "Molecular cloning of mouse tumour necrosis factor cDNA and its
RT   eukaryotic expression.";
RL   Nucleic Acids Res. 13:4417-4429(1985).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87298639; PubMed=3040015;
RA   Shakhov A.N., Nedospasov S.A.;
RT   "Molecular cloning of genes coding for tumor necrosis factor. Complete
RT   nucleotide sequence of the genome copy of TNF-alpha in mice.";
RL   Bioorg. Khim. 13:701-705(1987).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88067722; PubMed=3684584;
RA   Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
RT   "Nucleotide sequence of the murine TNF locus, including the TNF-alpha
RT   (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";
RL   Nucleic Acids Res. 15:9083-9084(1987).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CTS, and NOD;
RX   MEDLINE=96013654; PubMed=7560085;
RA   Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,
RA   Takekawa K., Ogihara T.;
RT   "Identification of a new susceptibility locus for insulin-dependent
RT   diabetes mellitus by ancestral haplotype congenic mapping.";
RL   J. Clin. Invest. 96:1936-1942(1995).
RN   [8]
RP   NUCLEOTIDE SEQUENCE, AND VARIANTS THR-7 AND ALA-77.
RC   STRAIN=A/J, BALB/c, and C57BL/6;
RX   MEDLINE=97246744; PubMed=9089109; DOI=10.1007/s002510050233;
RA   Iraqi F., Teale A.;
RT   "Cloning and sequencing of the Tnfa genes of three inbred mouse
RT   strains.";
RL   Immunogenetics 45:459-461(1997).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=129;
RX   PubMed=14656967; DOI=10.1101/gr.1736803;
RA   Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA   Campbell R.D., Hood L.;
RT   "Analysis of the gene-dense major histocompatibility complex class III
RT   region and its comparison to mouse.";
RL   Genome Res. 13:2621-2636(2003).
RN   [10]
RP   NUCLEOTIDE SEQUENCE OF 1-96.
RC   STRAIN=BFM/2Msf, BLG2/Msf, C57BL/10SnJ, CAST/Ei, HMI/Msf, MSM/Msf,
RC   NJL/Msf, pgn2, and SWN/Msf;
RA   Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
RT   "Conspicuous differences among gene genealogies of 21 nuclear genes of
RT   five Mus musculus subspecies.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   PROTEIN SEQUENCE OF 70-87.
RX   MEDLINE=89380231; PubMed=2777790;
RA   Cseh K., Beutler B.;
RT   "Alternative cleavage of the cachectin/tumor necrosis factor
RT   propeptide results in a larger, inactive form of secreted protein.";
RL   J. Biol. Chem. 264:16256-16260(1989).
RN   [12]
RP   PROTEIN SEQUENCE OF 80-99.
RX   MEDLINE=91097531; PubMed=2268312;
RA   Sherry B., Juc D.-M., Zentella A., Cerami A.;
RT   "Characterization of high molecular weight glycosylated forms of
RT   murine tumor necrosis factor.";
RL   Biochem. Biophys. Res. Commun. 173:1072-1078(1990).
RN   [13]
RP   IDENTIFICATION OF MEMBRANE-BOUND FORM.
RX   MEDLINE=88165056; PubMed=3349526;
RA   Kriegler M., Perez X., Defay K., Albert I., Lu S.D.;
RT   "A novel form of TNF/cachectin is a cell surface cytotoxic
RT   transmembrane protein: ramifications for the complex physiology of
RT   TNF.";
RL   Cell 53:45-53(1988).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.
RX   MEDLINE=99190964; PubMed=10089307; DOI=10.1107/S0907444998018435;
RA   Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;
RT   "The structure of mouse tumour-necrosis factor at 1.4 A resolution:
RT   towards modulation of its selectivity and trimerization.";
RL   Acta Crystallogr. D 55:772-778(1999).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing.
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; M20155; AAA40462.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; M11731; AAA40458.1; -; mRNA.
DR   EMBL; M13049; AAA40457.1; -; mRNA.
DR   EMBL; X02611; CAA26457.1; -; mRNA.
DR   EMBL; M38296; AAA40459.1; -; Genomic_DNA.
DR   EMBL; Y00467; CAA68530.1; -; Genomic_DNA.
DR   EMBL; U06950; AAA18594.1; -; Unassigned_DNA.
DR   EMBL; D84196; BAA19512.1; -; Genomic_DNA.
DR   EMBL; D84199; BAA19513.1; -; Genomic_DNA.
DR   EMBL; U68414; AAB65593.1; -; Genomic_DNA.
DR   EMBL; AF109719; AAC82484.1; -; Genomic_DNA.
DR   EMBL; AB039224; BAB68748.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039225; BAB68749.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039226; BAB68750.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039227; BAB68751.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039228; BAB68752.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039229; BAB68753.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039230; BAB68754.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039231; BAB68755.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AB039232; BAB68756.1; ALT_SEQ; Genomic_DNA.
DR   PIR; A22908; QWMSN.
DR   PDB; 2TNF; X-ray; A/B/C=80-235.
DR   Ensembl; ENSMUSG00000024401; Mus musculus.
DR   MGI; MGI:104798; Tnf.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0030141; C:secretory granule; TAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR   GO; GO:0006968; P:cellular defense response; TAS.
DR   GO; GO:0045123; P:cellular extravasation; IDA.
DR   GO; GO:0042742; P:defense response to bacteria; IDA.
DR   GO; GO:0007275; P:development; IMP.
DR   GO; GO:0006006; P:glucose metabolism; IDA.
DR   GO; GO:0006959; P:humoral immune response; IMP.
DR   GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; IGI.
DR   GO; GO:0048535; P:lymph node development; TAS.
DR   GO; GO:0046325; P:negative regulation of glucose import; IDA.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IDA.
DR   GO; GO:0006927; P:programmed cell death, transformed cells; TAS.
DR   GO; GO:0051023; P:regulation of immunoglobulin secretion; IDA.
DR   GO; GO:0045670; P:regulation of osteoclast differentiation; IDA.
DR   GO; GO:0001932; P:regulation of protein amino acid phosphoryl. . .; IDA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.

  Query Match             81.6%;  Score 641.5;  DB 1;  Length 235;
  Best Local Similarity   75.2%;  Pred. No. 4.1e-53;
  Matches  118;  Conservative   26;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:||||||| | | ||:||::|||||||||::|:|||||||::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||  :||||||:|| |:||| :||||||::||| ::|||||| :||||||||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:||:||||:| | |||||||||||||:|||
Db        199 GGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 31
Q3U593_MOUSE
ID   Q3U593_MOUSE   PRELIMINARY;   PRT;   235 AA.
AC   Q3U593;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A630097B05 product:tumor necrosis factor, full insert sequence
DE   (Activated spleen cDNA, RIKEN full-length enriched library,
DE   clone:F830002F15 product:tumor necrosis factor, full insert sequence)
DE   (Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830138A10 product:tumor necrosis factor, full insert sequence).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
```

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RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Bone marrow, and
RC   Thymus;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK153800; BAE32187.1; -; mRNA.
DR   EMBL; AK155964; BAE33525.1; -; mRNA.
DR   EMBL; AK153319; BAE31899.1; -; mRNA.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0030141; C:secretory granule; TAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IDA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR   GO; GO:0045123; P:cellular extravasation; IDA.
DR   GO; GO:0042742; P:defense response to bacteria; IDA.
DR   GO; GO:0007275; P:development; IMP.
DR   GO; GO:0006006; P:glucose metabolism; IDA.
DR   GO; GO:0006959; P:humoral immune response; IMP.
DR   GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; IGI.
DR   GO; GO:0046325; P:negative regulation of glucose import; IDA.
DR   GO; GO:0000122; P:negative regulation of transcription from R. . .; IDA.
DR   GO; GO:0009887; P:organ morphogenesis; IMP.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IDA.
DR   GO; GO:0045944; P:positive regulation of transcription from R. . .; IDA.
DR   GO; GO:0045994; P:positive regulation of translational initia. . .; IDA.
DR   GO; GO:0051023; P:regulation of immunoglobulin secretion; IDA.
DR   GO; GO:0045670; P:regulation of osteoclast differentiation; IDA.

  Query Match             81.6%;  Score 641.5;  DB 2;  Length 235;
  Best Local Similarity   75.2%;  Pred. No. 4.1e-53;
  Matches  118;  Conservative   26;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:||||||| | | ||:||::|||||||||::|:|||||||::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||  :||||||:|| |:||| :||||||::||| ::|||||| :||||||||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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                ||||||||:||:||||:| | ||||||||||||||:|||
Db        199 GGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL 235

RESULT 32
TNFA_CEREL
ID   TNFA_CEREL     STANDARD;      PRT;   229 AA.
AC   P51743;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-FEB-2006, entry version 38.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form]
DE   (Fragment).
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Lockhart E.A.;
RT   "Cloning and sequencing of cervine tumor necrosis factor.";
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U14683; AAA50759.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P51743; 82-229.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN        <1    229       Tumor necrosis factor, membrane form.
FT                                 /FTId=PRO_0000034415.
FT   CHAIN        74    229       Tumor necrosis factor, soluble form.
FT                                 /FTId=PRO_0000034416.
FT   TOPO_DOM     <1     30       Cytoplasmic (Potential).
FT   TRANSMEM     31     51       Signal-anchor for type II membrane
FT                                 protein (Potential).
FT   TOPO_DOM     52    229       Extracellular (Potential).
FT   SITE         72     73       Cleavage (by ADAM17) (By similarity).
FT   DISULFID    141    173       By similarity.
FT   NON_TER       1      1
SQ   SEQUENCE   229 AA;  24988 MW;  16DE5F7AA5A7DB35 CRC64;

  Query Match             81.4%;  Score 640;  DB 1;  Length 229;
  Best Local Similarity   78.3%;  Pred. No. 5.5e-53;
  Matches  123;  Conservative   18;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:   ::||||||||  |:||| ||:  ||||:||||:| |||||||::|||||||
Db         73 LRSSSQASINKPVAHVVANIAQGQLLWLDSCANALMANGVKLEDNQLVVPTDGLYLIYS 132

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|| |||| : |||||||||||||:||:||||:||| ||||| |||:|||||||
Db        133 QVLFRGQSCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 192

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| |||||:||||||||||||
Db        193 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 229

RESULT 33
TNFA_BOVIN
ID   TNFA_BOVIN     STANDARD;      PRT;   233 AA.
AC   Q06599; O18779; Q27978;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 1.
DT   07-FEB-2006, entry version 49.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94083525; PubMed=8260599; DOI=10.1016/1043-4666(93)90065-D;
RA   Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
RT   "Cloning and characterization of the tandemly arranged bovine
RT   lymphotoxin and tumour necrosis factor-alpha genes.";
RL   Cytokine 5:336-341(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Boran, and N'Dama;
RA   Iraqi F.;
RT   "Bovine TNF-alpha gene.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Ahn J.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 50-233.
RC   TISSUE=Blood;
RX   MEDLINE=96006582; PubMed=7590981; DOI=10.1007/BF00179409;
RA   Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT   "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RT   and tumor necrosis factor alpha.";
RL   Immunogenetics 42:430-431(1995).
RN   [5]
RP   NUCLEOTIDE SEQUENCE OF 89-193.
RC   STRAIN=Holstein;
RX   MEDLINE=97447737; PubMed=9303477;
RA   Dietz A.B., Neibergs H.L., Womack J.E., Kehrli M.E. Jr.;
RT   "Rapid communication: single strand conformational polymorphism (SSCP)
RT   of bovine tumor necrosis factor alpha.";
RL   J. Anim. Sci. 75:2567-2567(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
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CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; Z14137; CAA78511.1; -; Genomic_DNA.
DR   EMBL; AF011926; AAB84086.1; -; Genomic_DNA.
DR   EMBL; AF348421; AAN76506.1; -; mRNA.
DR   EMBL; AF011927; AAB84087.1; -; Genomic_DNA.
DR   EMBL; Z48808; CAA88743.1; -; mRNA.
DR   EMBL; U11040; AAA19573.1; ALT_SEQ; Unassigned_RNA.
DR   PIR; I46047; S24642.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q06599; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Polymorphism; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034403.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034404.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
FT   VARIANT      48     48       F -> C (in strain: N'Dama).
FT   CONFLICT     62     62       E -> EQ (in Ref. 3 and 4).
FT   CONFLICT    113    113       M -> V (in Ref. 3).
FT   CONFLICT    166    166       K -> R (in Ref. 3).
SQ   SEQUENCE   233 AA;  25439 MW;  8AF55C002A9763B0 CRC64;

  Query Match             81.3%;  Score 639;  DB 1;  Length 233;
  Best Local Similarity   77.7%;  Pred. No. 7e-53;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         77 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||| : |||||||||||||:||:||||:||| ||||| |||:|||||||
Db        137 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| |||||:||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 233
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RESULT 34
TNFA_BUBBU
ID   TNFA_BUBBU     STANDARD;      PRT;   233 AA.
AC   P59693;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Bubalus bubalis (Domestic water buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bubalus.
OX   NCBI_TaxID=89462;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   PubMed=15265025; DOI=10.1111/j.1365-2370.2004.00471.x;
RA   Gupta P.K., Bind R.B., Walunj S.S., Saini M.;
RT   "High nucleotide and amino acid sequence similarities in tumour
RT   necrosis factor-alpha amongst Indian buffalo (Bubalus bubalis), Indian
RT   cattle (Bos indicus) and other ruminants.";
RL   Eur. J. Immunogenet. 31:189-193(2004).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY221123; AAO62082.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P59693; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT                                /FTId=PRO_0000034405.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034406.
FT   TOPO_DOM      1     33       Cytoplasmic (Potential).
FT   TRANSMEM     34     56       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
```

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FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25413 MW;  E191191D81F326A4 CRC64;

  Query Match             81.3%;  Score 639;  DB 1;  Length 233;
  Best Local Similarity   77.7%;  Pred. No. 7e-53;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         77 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||| : |||||||||||||||:||:||||:||| ||||| |||:|||||||
Db        137 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:||||||||| |||||:|||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 233


RESULT 35
TNFA_BOSIN
ID   TNFA_BOSIN     STANDARD;      PRT;   234 AA.
AC   P59684;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Bos indicus (Zebu).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9915;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   PubMed=15265025; DOI=10.1111/j.1365-2370.2004.00471.x;
RA   Gupta P.K., Bind R.B., Walunj S.S., Saini M.;
RT   "High nucleotide and amino acid sequence similarities in tumour
RT   necrosis factor-alpha amongst Indian buffalo (Bubalus bubalis), Indian
RT   cattle (Bos indicus) and other ruminants.";
RL   Eur. J. Immunogenet. 31:189-193(2004).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY221122; AAO62081.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P59684; 83-234.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    234       Tumor necrosis factor, membrane form (By
FT                                 similarity).
FT                                 /FTId=PRO_0000034401.
FT   CHAIN        78    234       Tumor necrosis factor, soluble form (By
FT                                 similarity).
FT                                 /FTId=PRO_0000034402.
FT   TOPO_DOM      1     33       Cytoplasmic (Potential).
FT   TRANSMEM     34     56       Signal-anchor for type II membrane
FT                                 protein (By similarity).
FT   TOPO_DOM     57    234       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    146    178       By similarity.
SQ   SEQUENCE   234 AA;  25567 MW;  BAE4D0CD3797F491 CRC64;

  Query Match             81.3%;  Score 639;  DB 1;  Length 234;
  Best Local Similarity   77.7%;  Pred. No. 7e-53;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         78 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||| : |||||||||||||||:||:||||:||| ||||| |||:|||||||
Db        138 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:||||||||| |||||:|||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 234


RESULT 36
Q539C2_TUPTA
ID   Q539C2_TUPTA   PRELIMINARY;   PRT;   234 AA.
AC   Q539C2;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Tumor necrosis factor alpha.
GN   Name=TNF-alpha;
OS   Tupaia tana (Large tree shrew).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaia.
OX   NCBI_TaxID=70687;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lu M., Lu Y.;
RT   "Molecular characterization of Tupaia tana tumor necrosis factor
RT   alpha.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY610957; AAU11146.1; -; mRNA.
DR   SMR; Q539C2; 85-234.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002223; Prot_inh_Kunz-m.
DR   InterPro; IPR003638; TNF_8.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
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DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD023087; TNF_8; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; UNKNOWN_1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   234 AA;  25470 MW;  FE057E21F9CAF905 CRC64;

  Query Match             81.3%;  Score 639;  DB 2;  Length 234;
  Best Local Similarity   77.3%;  Pred. No. 7e-53;
  Matches  119;  Conservative   18;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          4 SSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              ||  |||:| |||:|||| :|:||||||||| || ||::| ||||||||:|||||||||
Db         81 SSGIPSDKPAAHVIANPQNKGELQWLNRRANTLLTNGMQLVDNQLVVPSDGLYLIYSQVL 140

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              |:| ||||| || |||:| :|||  :|||||||:||||:|| |||||:||||||| |||
Db        141 FTGLGCPSTPVLFTHTVSCVAVSYNNKVNLLSAIKSPCQKETAEGAEAKPWYEPIYQGGV 200

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||::|||||||:| | |||||||||||||:|||
Db        201 FQLQKGDRLSAEVNLPRYLDFAESGQVYFGVIAL 234


RESULT 37
Q2MGZ7_9CETA
ID   Q2MGZ7_9CETA   PRELIMINARY;   PRT;   234 AA.
AC   Q2MGZ7;
DT   21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   21-FEB-2006, sequence version 1.
DT   21-FEB-2006, entry version 1.
DE   Tumor Necrosis Factor-alpha.
GN   Name=TNF-a;
OS   Bubalus bubalis x Bubalus carabanensis.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bubalus.
OX   NCBI_TaxID=365610;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Mingala C.N., Raadan O., Konnai S., Ohashi K., Onuma M.;
RT   "Molecular cloning, sequencing and phylogenetic analysis of
RT   inflammatory cytokines of swamp type buffalo and some bubaline
RT   breeds.";
RL   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AB246793; BAE76015.1; -; mRNA.
SQ   SEQUENCE   234 AA;  25567 MW;  BAE4D0CD3797F491 CRC64;

  Query Match             81.3%;  Score 639;  DB 2;  Length 234;
  Best Local Similarity   77.7%;  Pred. No. 7e-53;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         78 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||| : |||||||||||||:||:||||:||| ||||| |||:|||||||
Db        138 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||| |||||:||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 234


RESULT 38
Q2MH01_BUBBU
ID   Q2MH01_BUBBU   PRELIMINARY;   PRT;   234 AA.
AC   Q2MH01;
DT   21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   21-FEB-2006, sequence version 1.
DT   21-FEB-2006, entry version 1.
DE   Tumor Necrosis Factor-alpha.
GN   Name=TNF-a;
OS   Bubalus bubalis (Domestic water buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bubalus.
OX   NCBI_TaxID=89462;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Mingala C.N., Raadan O., Konnai S., Ohashi K., Onuma M.;
RT   "Molecular cloning, sequencing and phylogenetic analysis of
RT   inflammatory cytokines of swamp type buffalo and some bubaline
RT   breeds.";
RL   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AB246789; BAE76011.1; -; mRNA.
SQ   SEQUENCE   234 AA;  25567 MW;  BAE4D0CD3797F491 CRC64;

  Query Match             81.3%;  Score 639;  DB 2;  Length 234;
  Best Local Similarity   77.7%;  Pred. No. 7e-53;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         78 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:||||||| : |||||||||||||:||:||||:||| ||||| |||:|||||||
Db        138 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||| |||||:||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 234


RESULT 39
Q2MH05_9CETA
ID   Q2MH05_9CETA   PRELIMINARY;   PRT;   234 AA.
AC   Q2MH05;
DT   21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT   21-FEB-2006, sequence version 1.
DT   21-FEB-2006, entry version 1.
DE   Tumor Necrosis Factor-alpha.
GN   Name=TNF-a;
OS   Bubalus carabanensis.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bubalus.
OX   NCBI_TaxID=346063;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Mingala C.N., Raadan O., Konnai S., Ohashi K., Onuma M.;
RT   "Molecular cloning, sequencing and phylogenetic analysis of
RT   inflammatory cytokines of swamp type buffalo and some bubaline
RT   breeds.";
RL   Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
```

```
DR   EMBL; AB246785; BAE76007.1; -; mRNA.
SQ   SEQUENCE   234 AA;  25567 MW;  BAE4D0CD3797F491 CRC64;

  Query Match             81.3%;  Score 639;  DB 2;  Length 234;
  Best Local Similarity   77.7%;  Pred. No. 7e-53;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |::|||||||:  : |||:| :  ||||:||||:| ||||||||::|||||||
Db         78 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||| : |||||||||||||:||:||||:||| ||||| |||:|||||||
Db        138 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||| |||||:||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 234


RESULT 40
TNFA_RABIT
ID   TNFA_RABIT     STANDARD;      PRT;   235 AA.
AC   P04924;
DT   13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT   13-AUG-1987, sequence version 1.
DT   07-FEB-2006, entry version 51.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91065534; PubMed=2249779; DOI=10.1016/0378-1119(90)90364-W;
RA   Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA   Nedospasov S.A.;
RT   "Structural analysis of the rabbit TNF locus, containing the genes
RT   encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT   factor).";
RL   Gene 95:215-221(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86219712; PubMed=3519138;
RA   Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
RA   Wallace R.B.;
RT   "Molecular cloning of the gene encoding rabbit tumor necrosis
RT   factor.";
RL   DNA 5:157-165(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86219711; PubMed=3519137;
RA   Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
RA   Hayashi H., Kato M., Seko M.;
RT   "Molecular cloning and expression in Escherichia coli of the cDNA
RT   coding for rabbit tumor necrosis factor.";
RL   DNA 5:149-156(1986).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; M12845; AAA31486.1; -; mRNA.
DR   EMBL; M12846; AAA31482.1; -; Genomic_DNA.
DR   EMBL; M60340; AAA31484.1; -; Genomic_DNA.
DR   PIR; A25454; A25451.
DR   HSSP; P06804; 2TNF.
DR   SMR; P04924; 88-235.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    235       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034449.
FT   CHAIN        80    235       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034450.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    235       Extracellular (Potential).
FT   SITE         79     80       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    148    179       By similarity.
FT   CONFLICT     63     63       Missing (in Ref. 3).
SQ   SEQUENCE   235 AA;  25817 MW;  610177D0BD2EF871 CRC64;

  Query Match             81.2%;  Score 638.5;  DB 1;  Length 235;
  Best Local Similarity   77.7%;  Pred. No. 7.9e-53;
  Matches  122;  Conservative   20;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||:||  ||:|:|||||||| |||||||::||||||.||::| |||||||::|||||||
Db         80 LRSASRALSDKPLAHVVANPQVEGQLQWLSQRANALLANGMKLTDNQLVVPADGLYLIYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||| | :||||||:|| ||||  :||||||:||| ||||| || : |||||||
Db        140 QVLFSGQGCRS-YVLLTHTVSRFAVSYPNKVNLLSAIKSPCHRETPEEAEPMAWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:||||| |:|:|:||| ||||||||||||
Db        199 GGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFGIIAL 235


RESULT 41
TNFA_SHEEP
ID   TNFA_SHEEP     STANDARD;      PRT;   234 AA.
AC   P23383;
DT   01-NOV-1991, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1994, sequence version 2.
DT   07-FEB-2006, entry version 48.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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OC   Pecora; Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Liver;
RX   MEDLINE=91067496; PubMed=2251151;
RA   Young A.J., Hay J.B., Chan J.Y.C.;
RT   "Primary structure of ovine tumor necrosis factor alpha cDNA.";
RL   Nucleic Acids Res. 18:6723-6723(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Alveolar macrophage;
RX   MEDLINE=92112044; PubMed=1765267; DOI=10.1016/0378-1119(91)90610-N;
RA   Green I.R., Sargan D.R.;
RT   "Sequence of the cDNA encoding ovine tumor necrosis factor-alpha:
RT   problems with cloning by inverse PCR.";
RL   Gene 109:203-210(1991).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92155784; PubMed=1786996;
RA   Andrews A.E., Nash A.D., Barcham G.J., Brandon M.R.;
RT   "Molecular cloning, expression and characterization of ovine TNF
RT   alpha.";
RL   Immunol. Cell Biol. 69:273-283(1991).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X55966; CAA39437.1; -; mRNA.
DR   EMBL; X55152; CAA38952.1; -; mRNA.
DR   EMBL; X56756; CAA40076.1; -; mRNA.
DR   EMBL; A19163; CAA01445.1; -; Unassigned_RNA.
DR   PIR; JH0529; JH0529.
DR   HSSP; P01375; 4TSV.
DR   SMR; P23383; 83-234.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Phosphorylation; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    234       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034455.
FT   CHAIN        78    234       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034456.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    234       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    146    178       By similarity.
FT   CONFLICT     63     63       Missing (in Ref. 1).
SQ   SEQUENCE   234 AA;  25536 MW;  4BCF8CCAB7956B88 CRC64;

  Query Match             81.0%;  Score 637;  DB 1;  Length 234;
  Best Local Similarity   77.7%;  Pred. No. 1.1e-52;
  Matches  122;  Conservative   20;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  :::||||||||  | |||:| :  ||||:||||||:||||||::|||||||
Db         78 LRSSSQASNNKPVAHVVANISAPGQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:| ||||| : |||||||||||||:||:||||:||| ||| |||||:|||||||
Db        138 QVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETLEGAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||||  |:|||:||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPEYLDYAESGQVYFGIIAL 234


RESULT 42
TNFA_PERLE
ID   TNFA_PERLE     STANDARD;      PRT;   235 AA.
AC   P36939;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 1.
DT   07-FEB-2006, entry version 43.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Peromyscus leucopus (White-footed mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Neotominae; Peromyscus.
OX   NCBI_TaxID=10041;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=92218012; PubMed=1348497; DOI=10.1007/BF00189900;
RA   Crew M.D., Filipowsky M.E.;
RT   "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
RT   Peromyscus leucopus (family Cricetidae).";
RL   Immunogenetics 35:351-353(1992).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M59233; AAA40596.1; -; Genomic_DNA.
DR   PIR; I54490; I54490.
DR   HSSP; P06804; 2TNF.
DR   SMR; P36939; 88-235.
```

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DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Phosphorylation; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    235       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034447.
FT   CHAIN        80    235       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034448.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    235       Extracellular (Potential).
FT   SITE         79     80       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   CARBOHYD     86     86       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    148    179       By similarity.
SQ   SEQUENCE   235 AA;  25823 MW;  235A5CFC9F9AC624 CRC64;

  Query Match             80.9%;  Score 635.5;  DB 1;  Length 235;
  Best Local Similarity   75.2%;  Pred. No. 1.5e-52;
  Matches  118;  Conservative   26;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:||||||| | : ||:||:| |||||||::|:|||||:|::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGANALLANGMDLKDNQLVIPADGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||| |::||||||:|| ||||: :|||||||:||| :|||||:| :||||||||
Db        140 QVLFKGQGC-SSYVLLTHTVSRFAVSYEDKVNLLSAIKSPCPKETPEGSELKPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||:| | ||||||||||||||:|||
Db        199 GGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 43
Q5W9H9_MERUN
ID   Q5W9H9_MERUN   PRELIMINARY;   PRT;   235 AA.
AC   Q5W9H9;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Tumor necrosis factor alpha.
GN   Name=TNFa;
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Gerbillinae; Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MGS/Sea; TISSUE=Macrophage;
RX   PubMed=15504246;
RA   Matsubara S., Shibata H., Takahashi M., Ishikawa F., Yokokura T.,
RA   Sugimura T., Wakabayashi K.;
RT   "Cloning of Mongolian gerbil cDNAs encoding inflammatory proteins, and
RT   their expression in glandular stomach during H. pylori infection.";
RL   Cancer Sci. 95:798-802(2004).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB177841; BAD67163.1; -; mRNA.
DR   SMR; Q5W9H9; 88-235.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   235 AA;  25786 MW;  C047E5816531818F CRC64;

  Query Match             80.2%;  Score 630.5;  DB 2;  Length 235;
  Best Local Similarity   77.1%;  Pred. No. 4.6e-52;
  Matches  121;  Conservative   18;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:|||||| | | | ||:||:|||||||||:||||||||||:||||:||
Db         80 LRSSSQNASDKPVAHVVPNHQVEEQLEWLSRRANALLANGMELRDNQLVVPSDGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||| :|||||   ||||||:|| ||||| :|:|||||:||| |: ||||| :||||||||
Db        140 QVLPKGQGCPHL-VLLTHTVSRFAVSYQDKVSLLSAIKSPCPRDAPEGAEPEPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||:| | ||||||  ||||||:|||
Db        199 GGVFQLEKGDRLSAEVNLPQYLDFAEPGQVYFGVIAL 235


RESULT 44
Q80XA4_PERMA
ID   Q80XA4_PERMA   PRELIMINARY;   PRT;   232 AA.
AC   Q80XA4;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor precursor (Fragment).
GN   Name=Tnf;
OS   Peromyscus maniculatus (Deer mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Neotominae; Peromyscus.
OX   NCBI_TaxID=10042;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Green R.M., Herbst M.M., Schountz T.;
RT   "Genomic organization of deer mouse (Peromyscus maniculatus) tumor
RT   necrosis factor.";
RL   Bios 75:12-17(2004).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY249143; AAP03078.1; -; Genomic_DNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q80XA4; 88-232.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
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DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Signal.
FT   SIGNAL        1     20       Potential.
FT   CHAIN         80    >232     tumor necrosis factor.
FT   NON_TER       232   232
SQ   SEQUENCE   232 AA;  25704 MW;  E48A9379DB4F216D CRC64;

  Query Match             80.1%;  Score 629.5;  DB 2;  Length 232;
  Best Local Similarity   75.3%;  Pred. No. 5.7e-52;
  Matches  116;  Conservative   25;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:||||||||| | : ||:||:||||||||||::|:|||||:|::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVDEQLEWLSRRANALLANGMDLKDNQLVIPADGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||| | :||||||:|| |||| : :||||||:||| :|||||:| :||||||||
Db        140 QVLFKGQGC-SNYVLLTHTVSRFAVSYEDKVNLLSAIKSPCPKETPEGSELKPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGI 154
              |||||||:||||||:| | ||||||||||||:
Db        199 GGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFGV 232


RESULT 45
TNFA_RAT
ID   TNFA_RAT       STANDARD;      PRT;   235 AA.
AC   P16599; Q9JI26; Q9JI27;
DT   01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT   01-AUG-1990, sequence version 1.
DT   07-FEB-2006, entry version 60.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=Tnf; Synonyms=Tnfa, Tnfsf2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Shirai T., Shimizu N., Horiguchi S., Ito H.;
RT   "Cloning and expression in Escherichia coli of the gene for rat tumor
RT   necrosis factor.";
RL   Agric. Biol. Chem. 53:1733-1736(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92329007; PubMed=1627266;
RA   Estler H.C., Grewe M., Gaussling R., Pavlovic M., Decker K.;
RT   "Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells
RT   and in vitro posttranslational processing based on a PCR-derived
RT   cDNA.";
RL   Biol. Chem. Hoppe-Seyler 373:271-281(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Testis;
RX   MEDLINE=94040766; PubMed=8224868; DOI=10.1016/0378-1119(93)90200-M;
RA   Kwon J., Chung I.Y., Benveniste E.N.;
RT   "Cloning and sequence analysis of the rat tumor necrosis factor-
RT   encoding genes.";
RL   Gene 132:227-236(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ACI/SegHsd, BB(DR)/Wor, Brown Norway/SsNHsd, DA/Bkl, F344/NHsd,
RC   and LEW/NHsd;
RX   MEDLINE=21369712; PubMed=11477479; DOI=10.1038/sj/gene/6363761;
RA   Furuya T., Joe B., Salstrom J.L., Hashiramoto A., Dobbins D.E.,
RA   Wilder R.L., Remmers E.F.;
RT   "Polymorphisms of the tumor necrosis factor alpha locus among
RT   autoimmune disease susceptible and resistant inbred rat strains.";
RL   Genes Immun. 2:229-232(2001).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Decker K.F.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE, AND VARIANTS PRO-122 AND GLU-190.
RC   STRAIN=Dark Agouti;
RA   Seidel M.F., Junier M.-P., Vetter H.;
RT   "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Brown Norway;
RX   PubMed=15060004; DOI=10.1101/gr.1987704;
RA   Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA   Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
RT   "The genomic sequence and comparative analysis of the rat major
RT   histocompatibility complex.";
RL   Genome Res. 14:631-639(2004).
RN   [8]
RP   NUCLEOTIDE SEQUENCE OF 1-231.
RC   TISSUE=Tail;
RA   Kirisits M.J., Vardimon D., Kunz H.W., Gill T.J. III;
RL   Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; D00475; BAA00367.1; -; Genomic_DNA.
DR   EMBL; X66539; CAA47146.1; -; mRNA.
DR   EMBL; L00981; AAA16275.1; -; Unassigned_DNA.
DR   EMBL; AF329982; AAK53568.1; -; Genomic_DNA.
DR   EMBL; AF329983; AAK53569.1; -; Genomic_DNA.
DR   EMBL; AF329984; AAK53570.1; -; Genomic_DNA.
DR   EMBL; AF329985; AAK53571.1; -; Genomic_DNA.
DR   EMBL; AF329986; AAK53572.1; -; Genomic_DNA.
DR   EMBL; AF329987; AAK53573.1; -; Genomic_DNA.
DR   EMBL; AJ002278; CAA05290.1; -; mRNA.
DR   EMBL; AF269159; AAF82567.1; -; mRNA.
DR   EMBL; AF269160; AAF82568.1; -; mRNA.
DR   EMBL; BX883046; CAE84003.1; -; Genomic_DNA.
DR   EMBL; L19123; AAA42255.1; -; Genomic_DNA.
DR   PIR; JU0029; JU0029.
DR   HSSP; P06804; 2TNF.
DR   SMR; P16599; 88-235.
DR   Ensembl; ENSRNOG00000000837; Rattus norvegicus.
DR   RGD; 3876; Tnf.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   GO; GO:0006917; P:induction of apoptosis; IDA.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0007165; P:signal transduction; IDA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
```

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DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Phosphorylation; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    235       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034451.
FT   CHAIN        80    235       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034452.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    235       Extracellular (Potential).
FT   SITE         79     80       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   CARBOHYD     86     86       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    148    179       By similarity.
FT   VARIANT     122    122       L -> P.
FT   VARIANT     190    190       K -> E.
FT   CONFLICT     39     39       L -> P (in Ref. 2 and 5).
FT   CONFLICT    163    163       I -> T (in Ref. 2 and 5).
FT   CONFLICT    202    202       F -> S (in Ref. 2 and 5).
SQ   SEQUENCE   235 AA;  25806 MW;  B808EC6D049C2F3B CRC64;

  Query Match             79.7%;  Score 626.5;  DB 1;  Length 235;
  Best Local Similarity   74.5%;  Pred. No. 1.1e-51;
  Matches  117;  Conservative   25;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:||||||| ||| ||:||::|||||||||::|:|||||||::|||||||
Db         80 LRSSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLIYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||  :||||||:|| |:||| :|:|||||:||| ::|||||| :|||||:||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPWYEPMYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|| ||||:| | |||  |||||||:|||
Db        199 GGVFQLEKGDLLSAEVNLPKYLDITESGQVYFGVIAL 235


RESULT 46
Q6EE11_RAT
ID   Q6EE11_RAT     PRELIMINARY;   PRT;   235 AA.
AC   Q6EE11;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Tumor necrosis factor alpha (Tumor necrosis factor superfamily, member
DE   2).
GN   Name=Tnf;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AUG/OlaHsd, PVG/OlaHsd, and WF/HanHsd;
RA   Warle M.C., van der Laan L.J.W., Kusters J.G., Pot R.G.J.,
RA   Segeren K.C.A., Ijzermans J.N.M., Metselaar H.J., Tilanus H.W.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Prostate;
RG   NIH MGC Project;
RL   Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY427674; AAR91625.1; -; Genomic_DNA.
DR   EMBL; AY427673; AAR91624.1; -; Genomic_DNA.
DR   EMBL; AY427675; AAR91626.1; -; Genomic_DNA.
DR   EMBL; BC107671; AAI07672.1; -; mRNA.
DR   SMR; Q6EE11; 88-235.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   235 AA;  25806 MW;  B808EC6D049C2F3B CRC64;

  Query Match             79.7%;  Score 626.5;  DB 2;  Length 235;
  Best Local Similarity   74.5%;  Pred. No. 1.1e-51;
  Matches  117;  Conservative   25;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:||||||| ||| ||:||::|||||||||::|:|||||||::|||||||
Db         80 LRSSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLIYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||  :||||||:|| |:||| :|:|||||:||| ::|||||| :|||||:||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPWYEPMYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|| ||||:| | |||  |||||||:|||
Db        199 GGVFQLEKGDLLSAEVNLPKYLDITESGQVYFGVIAL 235


RESULT 47
TNFA_CAMBA
ID   TNFA_CAMBA     STANDARD;      PRT;   233 AA.
AC   Q75N23;
DT   12-APR-2005, integrated into UniProtKB/Swiss-Prot.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
```

```
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Camelus bactrianus (Bactrian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
OC   Camelidae; Camelus.
OX   NCBI_TaxID=9837;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Odbileg R., Ohashi K., Onuma M.;
RT   "Cloning of inflammatory cytokine.";
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB178886; BAD18894.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q75N23; 86-232.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                 similarity).
FT                                 /FTId=PRO_0000034407.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                 similarity).
FT                                 /FTId=PRO_0000034408.
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                 protein (By similarity).
FT   TOPO_DOM     58    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25437 MW;  B4817C23020D9BB0 CRC64;

  Query Match             78.9%;  Score 620;  DB 1;  Length 233;
  Best Local Similarity   77.1%;  Pred. No. 4.7e-51;
  Matches  121;  Conservative   15;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:   |:|||||||:| |:|||||  | || ||||||:| |||||||::|||||||
Db         77 LRSSSQASRDKPVAHVVADPAAQGQLQWEKRFANTLLANGVKLEDNQLVVPTDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|| |||| | |||||||:|||| : ||||||:|||| | | |||:||||||||
Db        137 QVLFSGQRCPSTPVFLTHTISRLAVSYPNKANLLSAIKSPCQGGTSEEAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||: |||||||| |:||||||||||||||||
Db        197 GGVFQLEKDDRLSAEINMPNYLDFAESGQVYFGIIAL 233


RESULT 48
TNFA_LAMGL
ID   TNFA_LAMGL     STANDARD;      PRT;   233 AA.
AC   P59694;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   23-MAY-2003, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Lama glama (Llama).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Tylopoda;
OC   Camelidae; Lama.
OX   NCBI_TaxID=9844;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Odbileg R., Lee S.-I., Yoshida R., Chang K.-S., Ohashi K.,
RA   Sugimoto C., Onuma M.;
RT   "Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB107646; BAC75383.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P59694; 86-232.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                 similarity).
FT                                 /FTId=PRO_0000034425.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                 similarity).
```

```
FT                                /FTId=PRO_0000034426.
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     58    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25437 MW;  F5C07837505FBD86 CRC64;

  Query Match             78.9%;  Score 620;  DB 1;  Length 233;
  Best Local Similarity   77.1%;  Pred. No. 4.7e-51;
  Matches  121;  Conservative   15;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:   |:|||||||:| |:|||||  | || ||||||:| |||||||::|||||||
Db         77 LRSSSQASRDKPVAHVVADPAAQGQLQWEKRFANTLLANGVKLEDNQLVVPTDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|| |||| | |||||||:||||  : ||||||:||||  | | |||:||||||||
Db        137 QVLFSGQRCPSTPVFLTHTISRLAVSYPNKANLLSAIKSPCQGGTSEEAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||: |||||||| |:||||||||||||||||||
Db        197 GGVFQLEKDDRLSAEINMPNYLDFAESGQVYFGIIAL 233


RESULT 49
Q91ZL4_SIGHI
ID   Q91ZL4_SIGHI   PRELIMINARY;   PRT;   156 AA.
AC   Q91ZL4;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor alpha (Fragment).
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Sigmodontinae; Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22079879; PubMed=12085325; DOI=10.1086/340823;
RA   Blanco J.C., Richardson J.Y., Darnell M.E., Rowzee A., Pletneva L.M.,
RA   Porter D.D., Prince G.A.;
RT   "Cytokine and chemokine gene expression after primary and secondary
RT   respiratory syncytial virus infection in cotton rats.";
RL   J. Infect. Dis. 185:1780-1785(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14980081; DOI=10.1089/107999004772719873;
RA   Blanco J.C., Pletneva L.M., Boukhvalova M., Richardson J.Y.,
RA   Harris K.A., Prince G.A.;
RT   "The cotton rat: an underutilized animal model for human infectious
RT   diseases can now be exploited using specific reagents to cytokines,
RT   chemokines, and interferons.";
RL   J. Interferon Cytokine Res. 24:21-28(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Pletneva L.M., Bacot S., Blanco J.C., Langley R.J., Prince G.A.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF421388; AAL18818.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q91ZL4; 9-156.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   CHAIN        <1    156       tumor necrosis factor alpha.
FT   NON_TER       1      1
SQ   SEQUENCE   156 AA;  17303 MW;  DC565F3BC3C826E4 CRC64;

  Query Match             78.7%;  Score 618.5;  DB 2;  Length 156;
  Best Local Similarity   75.2%;  Pred. No. 3.8e-51;
  Matches  118;  Conservative   24;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:|||||||| ||| ||:||::|||||||||::||:||||:|::||||:||
Db          1 LRSSSQNLSDKPVAHVVANQQAEEQLEWLSQRANALLANGMDLRNNQLVIPADGLYLVYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:| |  |   |||||:|||||||: :|||||||:||| :|||:||| :||||||||
Db         61 QVLFKGLG-RSNCELLTHTVSRIAVSYEDKVNLLSAIKSPCPKETPQGAELKPWYEPIYL 119

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||:|||||||:| | ||||||||||||:|||
Db        120 GGVFQLEKGDRLSAEVNHPKYLDFAESGQVYFGVIAL 156


RESULT 50
TNFA_MARMO
ID   TNFA_MARMO     STANDARD;      PRT;   233 AA.
AC   O35734;
DT   15-JUL-1999, integrated into UniProtKB/Swiss-Prot.
DT   01-JAN-1998, sequence version 1.
DT   07-FEB-2006, entry version 40.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Sciuridae; Xerinae; Marmotini; Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=98139533; PubMed=9472070; DOI=10.1007/s002510050366;
RA   Lohrengel B., Lu M., Roggendorf M.;
RT   "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
RT   and IL-6.";
RL   Immunogenetics 47:332-335(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood;
RA   Zhou H., Hu J., Seeger C.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=20184748; PubMed=10721723; DOI=10.1016/S0378-1119(99)00494-1;
RA   Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
RT   "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
RT   structure, characterization and biological activity.";
RL   Gene 242:295-305(2000).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Hodgson P.D., Michalak T.I.;
RT   "Augmented hepatic interferon gamma expression and T cell influx
RT   characterize acute hepatitis progressing to recovery and residual
```

```
RT   lifelong virus persistence in experimental adult woodchuck hepatitis
RT   virus infection.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; Y14137; CAA74569.1; -; mRNA.
DR   EMBL; AF082491; AAC32615.1; -; mRNA.
DR   EMBL; AF012910; AAF34863.1; -; mRNA.
DR   EMBL; AF096268; AAF34867.1; -; Genomic_DNA.
DR   EMBL; AF333967; AAK52718.1; -; mRNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; O35734; 86-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034433.
FT   CHAIN        78    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034434.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    146    177       By similarity.
SQ   SEQUENCE   233 AA;  25765 MW;  34D3D1965DAAE0E7 CRC64;

  Query Match             77.8%;  Score 611.5;  DB 1;  Length 233;
  Best Local Similarity   74.5%;  Pred. No. 3.1e-50;
  Matches  117;  Conservative   23;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  :|:|||||||  : : || ||:||||||||||:|| |||||||: ||||:||
Db         78 LRSSSQNMNDKPVAHVVAKNEDKEQLVWLSRRANALLANGMELIDNQLVVPANGLYLVYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||| :||||||:|| ||||| :|||||||: ||| :|: |||| :||||||||
Db        138 QVLFKGQGCPS-YVLLTHTVSRFAVSYQDKVNLLSAIKSPCPKESLEGAEFKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||:|::|||||||:| | ||||||||||||:|||
Db        197 GGVFELQKGDRLSAEVNLPSYLDFAESGQVYFGVIAL 233


RESULT 51
Q6X658_MARMO
ID   Q6X658_MARMO   PRELIMINARY;   PRT;   233 AA.
AC   Q6X658;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Sciuridae; Xerinae; Marmotini; Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Wang Y., Jacob J.R., Menne S., Bellezza C.A., Tennant B.C.,
RA   Gerin J.L., Cote P.J.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY253724; AAP80576.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q6X658; 86-233.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   233 AA;  25765 MW;  75C3CA8C41C0E68B CRC64;

  Query Match             77.8%;  Score 611.5;  DB 2;  Length 233;
  Best Local Similarity   74.5%;  Pred. No. 3.1e-50;
  Matches  117;  Conservative   22;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  :|:|||||||  : : || ||:||||||||||:|| |||||||: ||||:||
Db         78 LRSSSQNMNDKPVAHVVAKNEDKEQLVWLSRRANALLANGMELIDNQLVVPANGLYLVYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||| |||||||:|| ||||| :|||||||: || :|: |||| :||||||||
Db        138 QVLFKGQGCPS-HVLLTHTVSRFAVSYQDKVNLLSAIKIPCPKESLEGAEFKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||:|::|||||||:| | ||||||||||||:|||
Db        197 GGVFELQKGDRLSAEVNLPSYLDFAESGQVYFGVIAL 233


RESULT 52
Q9BEC9_OCHPR
ID   Q9BEC9_OCHPR   PRELIMINARY;   PRT;   216 AA.
AC   Q9BEC9;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Ochotona princeps (Southern American pika).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Ochotonidae;
OC   Ochotona.
```

```
OX   NCBI_TaxID=9978;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286825; CAC28531.1; -; Genomic_DNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q9BEC9; 74-216.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     216    216
SQ   SEQUENCE   216 AA;  23848 MW;  31317D53D70B628D CRC64;

  Query Match             77.7%;  Score 610.5;  DB 2;  Length 216;
  Best Local Similarity   76.5%;  Pred. No. 3.5e-50;
  Matches  114;  Conservative   19;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||:||||||:|||||||||| ||||:|||:| |||||||::| ||||||| :||||:||
Db         69 LRSASRTPSDKPVAHVVANPQKEGQLEWLNQRLNALLANGLKLIDNQLVVPRDGLYLVYS 128

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|| ||| ::|||||:|| ||||  :|||||||:||||:||||| | : ||||||
Db        129 QVLFKGQACPS-YLLLTHTVSRFAVSYPNKVNLLSAIKSPCQKETPEGTEPMAWYEPIYQ 187

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |||||||:||||| |:| ||||| |||||
Db        188 GGVFQLEKGDRLSTEVNMPDYLDLAESGQ 216


RESULT 53
Q9BEE8_ERIEU
ID   Q9BEE8_ERIEU   PRELIMINARY;   PRT;   215 AA.
AC   Q9BEE8;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Erinaceus europaeus (Western European hedgehog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;
OC   Erinaceinae; Erinaceus.
OX   NCBI_TaxID=9365;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286830; CAC28522.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9BEE8; 72-215.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     215    215
SQ   SEQUENCE   215 AA;  23696 MW;  3E337E7E65F074EA CRC64;

  Query Match             77.2%;  Score 607;  DB 2;  Length 215;
  Best Local Similarity   80.1%;  Pred. No. 7.5e-50;
  Matches  117;  Conservative   13;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 SSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              |||| ||:|||||||: ::|||| | :  |||||||::| ||||||| :||||||||||
Db         70 SSRTQSDKPVAHVVASIKSEGQLLWESEVANALLANGMKLTDNQLVVPLDGLYLIYSQVL 129

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              |:||||||||| ||| | | ||||| :|||||||:|||| ||||||||:||||||||||
Db        130 FKGQGCPSTHVFLTHNIKRYAVSYQKDVNLLSAIKSPCQSETPEGAEARPWYEPIYLGGV 189

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQ 149
              ||||:||||||||| |||||| ||||
Db        190 FQLEKGDRLSAEINLPDYLDFDESGQ 215


RESULT 54
O70332_MESAU
ID   O70332_MESAU   PRELIMINARY;   PRT;   216 AA.
AC   O70332;
DT   01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT   01-AUG-1998, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Tumor necrosis factor-alpha (Fragment).
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=98234044; PubMed=9573100;
RA   Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT   "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT   analysis of cytokine mRNA expression in experimental visceral
RT   leishmaniasis.";
RL   Infect. Immun. 66:2135-2142(1998).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF046215; AAC40100.1; -; mRNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; O70332; 78-216.
```

```
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     216    216
SQ   SEQUENCE   216 AA;  23793 MW;  BADAE3F83F45B533 CRC64;

  Query Match             75.9%;  Score 596.5;  DB 2;  Length 216;
  Best Local Similarity   75.0%;  Pred. No. 7.8e-49;
  Matches  111;  Conservative   22;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  :|:|| ||||| | | ||:||: |||||||||: |:|||||:|::||||:||
Db         70 LRSSSQNSNDKPVGHVVANHQVEEQLEWLSHRANALLANGMSLKDNQLVIPADGLYLVYS 129

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||||| :||||||:|||||||: :|||||||:||| :||||| | :||||||||
Db        130 QVLFRGQGCPS-YVLLTHTVSRIAVSYEDNVNLLSAIKSPCPKETPEGEELKPWYEPIYL 188

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESG 148
              |||||||:|||||||:| | ||||||||
Db        189 GGVFQLEKGDRLSAEVNLPKYLDFAESG 216


RESULT 55
Q9ERG6_PERMA
ID   Q9ERG6_PERMA   PRELIMINARY;   PRT;   217 AA.
AC   Q9ERG6;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor alpha (Fragment).
OS   Peromyscus maniculatus (Deer mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Neotominae; Peromyscus.
OX   NCBI_TaxID=10042;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=21987907; PubMed=11991673; DOI=10.1006/cyto.2001.0998;
RA   Herbst M.M., Prescott J., Palmer A.D., Schountz T.;
RT   "Sequence and expression analysis of deer mouse interferon-gamma,
RT   interleukin-10, tumor necrosis factor, and lymphotoxin-alpha.";
RL   Cytokine 17:203-213(2002).
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF307013; AAG30264.1; -; mRNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q9ERG6; 80-217.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     217    217
SQ   SEQUENCE   217 AA;  23964 MW;  D6F90C74C0B3021F CRC64;

  Query Match             75.4%;  Score 592.5;  DB 2;  Length 217;
  Best Local Similarity   74.8%;  Pred. No. 1.9e-48;
  Matches  110;  Conservative   24;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:|||||||| | : ||:||:||||||||||::|:|||||:|::||||:||
Db         72 LRSSSQNSSDKPVAHVVANHQVDEQLEWLSRRANALLANGMDLKDNQLVIPADGLYLVYS 131

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||| | :||||||:|| |||||: :|||||||:||| :|||||:| :||||||||
Db        132 QVLFKGQGC-SNYVLLTHTVSRFAVSYEDKVNLLSAIKSPCPKETPEGSELKPWYEPIYL 190

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAES 147
              |||||||:|||||||:| | |||||||
Db        191 GGVFQLEKGDRLSAEVNLPKYLDFAES 217


RESULT 56
Q9BEC5_TENEC
ID   Q9BEC5_TENEC   PRELIMINARY;   PRT;   217 AA.
AC   Q9BEC5;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Tenrec ecaudatus (Common tenrec).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Afrotheria; Tenrecidae; Tenrecinae; Tenrec.
OX   NCBI_TaxID=94439;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286826; CAC28538.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9BEC5; 74-217.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     217    217
SQ   SEQUENCE   217 AA;  23845 MW;  1C5013E9B777B54A CRC64;
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  Query Match           75.2%;  Score 591;  DB 2;  Length 217;
  Best Local Similarity   75.2%;  Pred. No. 2.6e-48;
  Matches  112;  Conservative   21;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||| ||:|||||||: | ||||:|::: ||||| | |:| ||||||| :|||||||
Db         69 LRSSSRTLSDKPVAHVVASTQDEGQLKWVSKVANALLDNNVQLIDNQLVVPLDGLYLIYS 128

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:| ||  |:|:||||:|||||||| :|||||||::|| ||||||:| :||||||||
Db        129 QVLFKGPGCHGTYVILTHTVSRIAVSYQAKVNLLSAIKTPCHRETPEGSETKPWYEPIYL 188

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              ||||||::||||||||| |:||| |||||
Db        189 GGVFQLQKGDRLSAEINLPNYLDLAESGQ 217


RESULT 57
Q99ND1_SCIVU
ID   Q99ND1_SCIVU   PRELIMINARY;   PRT;   215 AA.
AC   Q99ND1;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Sciurus vulgaris (Red squirrel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Sciuridae; Sciurinae; Sciurini; Sciurus.
OX   NCBI_TaxID=55149;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286824; CAC28540.1; -; Genomic_DNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q99ND1; 77-215.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     215    215
SQ   SEQUENCE   215 AA;  23739 MW;  36441309CA5E9898 CRC64;

  Query Match           74.3%;  Score 584;  DB 2;  Length 215;
  Best Local Similarity   76.5%;  Pred. No. 1.2e-47;
  Matches  114;  Conservative   21;  Mismatches   12;  Indels    2;  Gaps    2;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  :|:|||||||| | | |||||:||||||||||:|| |||||||::|||||||
Db         69 LRSSSQNMNDKPVAHVVAN-QTEEQLQWLSRRANALLANGMELIDNQLVVPADGLYLIYS 127

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              ||||:|||| |::|||||||:|| ||||| :|||||||:||| :|: |||| :||||||||
Db        128 QVLFKGQGC-SSYVLLTHTVSRFAVSYQDKVNLLSAIKSPCPKESLEGAEFKPWYEPIYL 186

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              `|||:|::|||||||:| | |||||||||
Db        187 GGVFELQKGDRLSAEVNLPSYLDFAESGQ 215


RESULT 58
TNFA_MACEU
ID   TNFA_MACEU     STANDARD;      PRT;   233 AA.
AC   O77764;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1998, sequence version 1.
DT   07-FEB-2006, entry version 34.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=99216446; PubMed=10199924; DOI=10.1007/s002510050521;
RA   Harrison G.A., Broughton M.J., Young L.J., Cooper D.W., Deane E.M.;
RT   "Conservation of 3' untranslated region elements in tammar wallaby
RT   (Macropus eugenii) TNF-alpha mRNA.";
RL   Immunogenetics 49:464-467(1999).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF055915; AAC61491.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O77764; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034427.
FT   CHAIN        78    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034428.
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FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (Potential).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25697 MW;  90AFFD137AF4E348 CRC64;

  Query Match             74.3%;  Score 584;  DB 1;  Length 233;
  Best Local Similarity   69.5%;  Pred. No. 1.4e-47;
  Matches  107;  Conservative   28;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          4 SSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              | :| |::|||||:|:| |||:|||| |||| ||:||::| |||||||| ||||:|||:|
Db         80 SCQTESNKPVAHVIADPLAEGKLQWLKRRANVLLSNGMDLVDNQLVVPSTGLYLVYSQLL 139

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              |:|: | :  :|||||:||:|:|||::|||||||:||||:      ||:||||||||||
Db        140 FKGEDCANEPLLLTHTVSRVALSYQSKVNLLSAIKSPCQKTVKGAREASPWYEPIYLGGV 199

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||:||:|||: | |:|||||||||||||:|||
Db        200 FQLEKGDKLSADTNYPNYLDFAESGQVYFGVIAL 233


RESULT 59
Q3T4H5_MACEU
ID   Q3T4H5_MACEU   PRELIMINARY;   PRT;   233 AA.
AC   Q3T4H5;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Tumour necrosis factor alpha.
GN   Name=TFN;
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=16103651; DOI=10.1159/000086379;
RA   Cross J.G., Harrison G.A., Coggill P., Sims S., Beck S., Deakin J.E.,
RA   Graves J.A.;
RT   "Analysis of the genomic region containing the tammar wallaby
RT   (Macropus eugenii) orthologues of MHC class III genes.";
RL   Cytogenet. Genome Res. 111:110-117(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Harrison G.G., Cross J.G., Deakin J.E., Marshall Graves J.A.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY853666; AAZ99793.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   233 AA;  25667 MW;  46782663674231DF CRC64;

  Query Match             74.3%;  Score 584;  DB 2;  Length 233;
  Best Local Similarity   69.5%;  Pred. No. 1.4e-47;
  Matches  107;  Conservative   28;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          4 SSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              | :| |::|||||:|:| |||:|||| |||| ||:||::| |||||||| ||||:|||:|
Db         80 SCQTESNKPVAHVIADPLAEGKLQWLKRRANVLLSNGMDLVDNQLVVPSTGLYLVYSQLL 139

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              |:|: | :  :|||||:||:|:|||::|||||||:||||:      ||:||||||||||
Db        140 FKGEDCANEPLLLTHTVSRVALSYQSKVNLLSAIKSPCQKTVKGAREASPWYEPIYLGGV 199

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||:||:|||: | |:|||||||||||||:|||
Db        200 FQLEKGDKLSADTNYPNYLDFAESGQVYFGVIAL 233


RESULT 60
Q3U4I6_MOUSE
ID   Q3U4I6_MOUSE   PRELIMINARY;   PRT;   219 AA.
AC   Q3U4I6;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched
DE   library, clone:F630010J11 product:tumor necrosis factor, full insert
DE   sequence.
GN   Name=Tnf;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
```

RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC ---

CC ---
DR EMBL; AK154223; BAE32445.1; -; mRNA.
DR MGI; MGI:104798; Tnf.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0030141; C:secretory granule; TAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IDA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR GO; GO:0045123; P:cellular extravasation; IDA.
DR GO; GO:0042742; P:defense response to bacteria; IDA.
DR GO; GO:0007275; P:development; IMP.
DR GO; GO:0006006; P:glucose metabolism; IDA.
DR GO; GO:0006959; P:humoral immune response; IMP.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; IGI.
DR GO; GO:0046325; P:negative regulation of glucose import; IDA.
DR GO; GO:0000122; P:negative regulation of transcription from R. . .; IDA.
DR GO; GO:0009887; P:organ morphogenesis; IMP.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IDA.
DR GO; GO:0045944; P:positive regulation of transcription from R. . .; IDA.
DR GO; GO:0045994; P:positive regulation of translational initia. . .; IDA.
DR GO; GO:0051023; P:regulation of immunoglobulin secretion; IDA.
DR GO; GO:0045670; P:regulation of osteoclast differentiation; IDA.
DR GO; GO:0001932; P:regulation of protein amino acid phosphoryl. . .; IDA.
DR GO; GO:0006927; P:transformed cell apoptosis; TAS.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR002959; TNF_alpha.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.

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  Query Match            73.3%;  Score 576.5;  DB 2;  Length 219;
  Best Local Similarity   68.6%;  Pred. No. 6.7e-47;
  Matches  107;  Conservative   27;  Mismatches   15;  Indels    7;  Gaps    2;

Qy          8 PSDXPVAHVVA------NPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
              |: :|:   :|      | | ||:||::|||||||||::|:|||||||::||||:|||
Db         65 PNGLPLISSMAQTLTLTNHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQ 124

Qy         62 VLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLG 121
              |||:|||||  :|||||:||  |:|||  :||||||::|||  ::|||||| :|||||||||
Db        125 VLFKGQGCPD-YVLLTHAVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYLG 183

Qy        122 GVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||:||:||||:| | |||||||||||||:|||
Db        184 GVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL 219


RESULT 61
Q9BEE0_MACRU
ID   Q9BEE0_MACRU   PRELIMINARY;   PRT;   216 AA.
AC   Q9BEE0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
OS   Macropus rufus (Red kangaroo) (Megaleia rufa).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286833; CAC28527.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9BEE0; 73-216.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     216    216
SQ   SEQUENCE   216 AA;  23829 MW;  3AF7E646B2D4AF6D CRC64;

  Query Match            69.5%;  Score 546;  DB 2;  Length 216;
  Best Local Similarity   68.5%;  Pred. No. 5.6e-44;
  Matches  100;  Conservative   27;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          4 SSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              | :| |::|||||:|:| |||:|||| |||| ||:||::| |||||||| ||||:|||:|
Db         71 SCQTESNKPVAHVIADPLAEGKLQWLKRRANVLLSNGMDLVDNQLVVPSTGLYLVYSQLL 130

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              |:|: | :  :|||||:||:|:|||::|||||||:||||:      ||:||||||||||
Db        131 FKGEDCANEPLLLTHTVSRVALSYQSKVNLLSAIKSPCQKTVKGAREASPWYEPIYLGGV 190

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQ 149
              ||||:||:|||: | |:|||||||||
Db        191 FQLEKGDKLSADTNYPNYLDFAESGQ 216


RESULT 62
Q8HZD8_9PRIM
ID   Q8HZD8_9PRIM   PRELIMINARY;   PRT;   155 AA.
AC   Q8HZD8;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor (Fragment).
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   O'hUigin C., Tichy H., Klein J.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY091965; AAM76583.1; -; Genomic_DNA.
DR   HSSP; P01375; 1TNF.
DR   SMR; Q8HZD8; 53-155.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     155    155
SQ   SEQUENCE   155 AA;  16924 MW;  32FB06B9717EF38E CRC64;

  Query Match            68.6%;  Score 539;  DB 2;  Length 155;
  Best Local Similarity   94.6%;  Pred. No. 1.7e-43;
  Matches  105;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||::|||||||||||||||||||||||||||||||||||||||||||||||||
Db         45 VRSSSRTPSBKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 104

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEA 111
              ||||:|||||||||||||||||||||:|||||||:|||||  ||||||
Db        105 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQREYPEGAEA 155


RESULT 63
Q8HZD7_PONPY
ID   Q8HZD7_PONPY   PRELIMINARY;   PRT;   155 AA.
AC   Q8HZD7;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor (Fragment).
OS   Pongo pygmaeus (Orangutan).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   O'hUigin C., Tichy H., Klein J.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY091966; AAM76584.1; -; Genomic_DNA.
DR   HSSP; P01375; 1TNF.
DR   SMR; Q8HZD7; 53-155.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     155    155
SQ   SEQUENCE   155 AA;  16790 MW;  D561099968693862 CRC64;

  Query Match             68.4%;  Score 538;  DB 2;  Length 155;
  Best Local Similarity   94.6%;  Pred. No. 2.1e-43;
  Matches  105;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||::|||||||||||||||||||||||||||||||||||||||||||||||||
Db         45 VRSSSRTPSBKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 104

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEA 111
              ||||:|||||||||||||||||||||||:|||||||:|||||| |||||
Db        105 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETTEGAEA 155


RESULT 64
Q8HZD5_SAGOE
ID   Q8HZD5_SAGOE   PRELIMINARY;   PRT;   155 AA.
AC   Q8HZD5;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Tumor necrosis factor (Fragment).
OS   Saguinus oedipus (Cotton-top tamarin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
OC   Callitrichidae; Saguinus.
OX   NCBI_TaxID=9490;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   O'hUigin C., Tichy H., Klein J.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY091968; AAM76586.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8HZD5; 50-154.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     155    155
SQ   SEQUENCE   155 AA;  16766 MW;  C9F485F0AD338958 CRC64;

  Query Match             64.8%;  Score 509;  DB 2;  Length 155;
  Best Local Similarity   89.1%;  Pred. No. 1.3e-40;
  Matches   98;  Conservative    9;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||| |||:||||||||||||||||||||||||||||||||||||||||||||:||
Db         45 VRSSSRIPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLVYS 104

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAE 110
              ||||:||||||| :||||:||||||||| :||||||||:||||||||:||:
Db        105 QVLFKGQGCPSTFMLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPQGAK 154


RESULT 65
Q864Z0_PHYCA
ID   Q864Z0_PHYCA   PRELIMINARY;   PRT;   103 AA.
AC   Q864Z0;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Physeter catodon (Sperm whale) (Physeter macrocephalus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC   Odontoceti; Physeteridae; Physeter.
OX   NCBI_TaxID=9755;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550766; CAD80053.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q864Z0; 1-103.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
```

```
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     103    103
SQ   SEQUENCE   103 AA;  11515 MW;  1BAEB2D43F5F2F38 CRC64;

  Query Match             61.8%;  Score 486;  DB 2;  Length 103;
  Best Local Similarity   88.3%;  Pred. No. 1.3e-38;
  Matches   91;  Conservative    8;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         47 QLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP 106
              |||||::|||||||||||:||||| ||: |||||||||||||:|||||||:||||||||
Db          1 QLVVPTDGLYLIYSQVLFRGQGCPPTHLFLTHTISRIAVSYQTKVNLLSAIKSPCQRETP 60

Qy        107 EGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |||||:||||||| |||||||:||||||||| ||||||||||
Db         61 EGAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPDYLDFAESGQ 103


RESULT 66
Q864Y9_9EUTH
ID   Q864Y9_9EUTH   PRELIMINARY;   PRT;   103 AA.
AC   Q864Y9;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Manis sp. CP2002.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Pholidota; Manidae; Manis.
OX   NCBI_TaxID=189736;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550767; CAD80054.1; -; Genomic_DNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q864Y9; 1-103.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     103    103
SQ   SEQUENCE   103 AA;  11431 MW;  21ADDEE6C8CD13DE CRC64;

  Query Match             60.9%;  Score 479;  DB 2;  Length 103;
  Best Local Similarity   86.4%;  Pred. No. 5.9e-38;
  Matches   89;  Conservative    9;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         47 QLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP 106
              ||||||:||||:||||||:||||||||||||||||:|:||||:|||||||:|||| |||
Db          1 QLVVPSDGLYLVYSQVLFKGQGCPSTHVLLTHTISRLALSYQTKVNLLSAIKSPCQLETP 60

Qy        107 EGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              || | :|||||||||||||||: |||||||| ||||||||||
Db         61 EGTEGKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQ 103


RESULT 67
Q864Y8_ELEMA
ID   Q864Y8_ELEMA   PRELIMINARY;   PRT;   99 AA.
AC   Q864Y8;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Elephas maximus (Indian elephant).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Afrotheria; Proboscidea; Elephantidae; Elephas.
OX   NCBI_TaxID=9783;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550768; CAD80055.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q864Y8; 1-99.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER      99     99
SQ   SEQUENCE   99 AA;  11005 MW;  FA06596C8CF33EFD CRC64;

  Query Match             59.0%;  Score 464;  DB 2;  Length 99;
  Best Local Similarity   87.9%;  Pred. No. 1.6e-36;
  Matches   87;  Conservative    8;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 PSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAE 110
              | :|||||||||||:|||||:| |||||||||||||:|:|||||||:||| ||||||||
Db          1 PFDGLYLIYSQVLFKGQGCPATQVLLTHTISRIAVSYKTKVNLLSAIKSPCHRETPEGAE 60

Qy        111 AXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |:|||||||||||||:||||||||| ||||||||||
Db         61 AKPWYEPIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQ 99


RESULT 68
Q9BEF3_DIDMA
ID   Q9BEF3_DIDMA   PRELIMINARY;   PRT;   214 AA.
AC   Q9BEF3;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (Fragment).
GN   Name=tnfa;
```

```
OS   Didelphis marsupialis virginiana (North American opossum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX   NCBI_TaxID=9267;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.M., de Jong W.W.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   van Dijk M.A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ286832; CAC28519.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     214    214
SQ   SEQUENCE   214 AA;  23594 MW;  E985D0D8A87E49E7 CRC64;

  Query Match             58.6%;  Score 460.5;  DB 2;  Length 214;
  Best Local Similarity   60.3%;  Pred. No. 9.5e-36;
  Matches   88;  Conservative   27;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          4 SSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              | :: |::|||||||   :| ::|| :  || || ||:|| |||||||: ||||:|||||
Db         70 SYQSESNKPVAHVVARTISEDKIQWSSGHANDLL-NGIELTDNQLVVPATGLYLVYSQVL 128

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              |:|: | :  ::||||:||:| ||  :||||:||:|||||       |::||||||||||
Db        129 FKGKDCANKPLILTHTVSRVARSYPDKVNLLAAIKSPCQRVEKGSGESNPWYEPIYLGGV 188

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQ 149
              ||||:|| ||:: | | ||| ||:||
Db        189 FQLEKGDMLSSDTNYPTYLDIAETGQ 214


RESULT 69
Q80Z02_9HYST
ID   Q80Z02_9HYST   PRELIMINARY;   PRT;   102 AA.
AC   Q80Z02;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Trichys fasciculata (long-tailed porcupine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC   Hystricognathi; Hystricidae; Trichys.
OX   NCBI_TaxID=73865;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550774; CAD80061.1; -; Genomic_DNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q80Z02; 1-102.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     102    102
SQ   SEQUENCE   102 AA;  11323 MW;  D935CDFA8FEDFCEF CRC64;

  Query Match             58.5%;  Score 459.5;  DB 2;  Length 102;
  Best Local Similarity   83.5%;  Pred. No. 4.4e-36;
  Matches   86;  Conservative   13;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         47 QLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP 106
              ||||||:||||||||||:|||||| :||||||:||:||||| :||||||:||||:|||
Db          1 QLVVPSDGLYLIYSQVLFKGQGCPS-YVLLTHTVSRLAVSYQDKVNLLSAIKSPCQKETP 59

Qy        107 EGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |||| :||||||||||||::|||||||:| |:|||||||||
Db         60 EGAELKPWYEPIYLGGVFQLQKGDRLSAEVNLPNYLDFAESGQ 102


RESULT 70
Q80Z03_CASCN
ID   Q80Z03_CASCN   PRELIMINARY;   PRT;   102 AA.
AC   Q80Z03;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Castor canadensis (Beaver).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Castoridae; Castor.
OX   NCBI_TaxID=51338;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
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DR   EMBL; AJ550773; CAD80060.1; -; Genomic_DNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q80Z03; 1-102.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
```

```
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     102    102
SQ   SEQUENCE   102 AA;  11343 MW;  77B343F6F598F0B1 CRC64;

  Query Match             57.6%;  Score 452.5;  DB 2;  Length 102;
  Best Local Similarity   82.5%;  Pred. No. 2.1e-35;
  Matches   85;  Conservative   12;  Mismatches    5;  Indels    1;  Gaps    1;

Qy         47 QLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP 106
              |||||::|||||||||||:|||||| :||||||:|| |||| : |||||||:||||:|||
Db          1 QLVVPADGLYLIYSQVLFKGQGCPS-YVLLTHTVSRFAVSYRENVNLLSAIKSPCQKETP 59

Qy        107 EGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |||| :|||||||||||||||:|||||||:| | |||||||||
Db         60 EGAELKPWYEPIYLGGVFQLEKGDRLSAEVNLPSYLDFAESGQ 102


RESULT 71
Q95LE8_CANFA
ID   Q95LE8_CANFA   PRELIMINARY;   PRT;    99 AA.
AC   Q95LE8;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   TNF-alpha (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   MEDLINE=21589073; PubMed=11730929; DOI=10.1016/S0165-2427(01)00385-3;
RA   Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT   "Semi-quantitative analysis of multiple cytokines in canine peripheral
RT   blood mononuclear cells by [correction of zby] a single tube RT-PCR.";
RL   Vet. Immunol. Immunopathol. 83:191-202(2001).
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CC   ---------------------------------------------------------------------
DR   EMBL; AF327899; AAL26919.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q95LE8; 7-99.
DR   Ensembl; ENSCAFG00000000517; Canis familiaris.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER      99     99
SQ   SEQUENCE   99 AA;  10760 MW;  3977AE499F00D7B0 CRC64;

  Query Match             57.5%;  Score 452;  DB 2;  Length 99;
  Best Local Similarity   88.8%;  Pred. No. 2.2e-35;
  Matches   87;  Conservative    9;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |:||||||||:|||||||||:||||||||:|||||||||||| ||||:|||:|||||||
Db          2 VKSSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLIVPSDGLYLIYS 61

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIX 98
              ||||:|||||||||||||||| ||||||:|||||||:
Db         62 QVLFKGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIK 99


RESULT 72
Q80Z04_9RODE
ID   Q80Z04_9RODE   PRELIMINARY;   PRT;   102 AA.
AC   Q80Z04;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Anomalurus sp. T-1787.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Anomaluridae; Anomalurus.
OX   NCBI_TaxID=131388;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550772; CAD80059.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q80Z04; 1-102.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     102    102
SQ   SEQUENCE   102 AA;  11295 MW;  637C8C21E7F29BED CRC64;

  Query Match             56.4%;  Score 443.5;  DB 2;  Length 102;
  Best Local Similarity   81.6%;  Pred. No. 1.5e-34;
  Matches   84;  Conservative   11;  Mismatches    7;  Indels    1;  Gaps    1;

Qy         47 QLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP 106
              |||||: |||||||||||:|||||| :|||||:|||||||  :||||||:|||:|||
```

```
Db          1 QLVVPTNGLYLIYSQVLFKGQGCPS-FMLLTHTVSRIAVSYPEKVNLLSAIKSPCQKETP 59

Qy        107 EGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |||: :|||||||||||||||:|||||||:| | |||||||||
Db         60 EGADLKPWYEPIYLGGVFQLEKGDRLSAEVNLPSYLDFAESGQ 102


RESULT 73
Q80Z06_DIPSA
ID   Q80Z06_DIPSA   PRELIMINARY;   PRT;   102 AA.
AC   Q80Z06;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Dipus sagitta (Northern three-toed jerboa).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Dipodidae; Dipodinae; Dipus.
OX   NCBI_TaxID=73863;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550770; CAD80057.1; -; Genomic_DNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q80Z06; 1-102.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
FT   NON_TER     102     102
SQ   SEQUENCE   102 AA;  11205 MW;  346023978DCCCA6C CRC64;

  Query Match             56.2%;  Score 441.5;  DB 2;  Length 102;
  Best Local Similarity   79.6%;  Pred. No. 2.4e-34;
  Matches   82;  Conservative   13;  Mismatches    7;  Indels    1;  Gaps    1;

Qy         47 QLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP 106
              ||||||:||||:||||||:|||||| :||||||:|| | ||  :|||||||:||| :||
Db          1 QLVVPSDGLYLVYSQVLFKGQGCPS-YVLLTHTVSRFAASYPDKVNLLSAIKSPCPKETS 59

Qy        107 EGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              ||||::|||||:|||||||||:|||||||:| ||||||||||
Db         60 EGAESKPWYEPVYLGGVFQLEKGDRLSAEVNLPDYLDFAESGQ 102


RESULT 74
TNFA_TRIVU
ID   TNFA_TRIVU     STANDARD;      PRT;   233 AA.
AC   P79374;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1997, sequence version 1.
DT   07-FEB-2006, entry version 35.
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Trichosurus vulpecula (Brush-tailed possum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX   NCBI_TaxID=9337;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=96315690; PubMed=8724002;
RA   Wedlock D.N., Aldwell F.E., Buddle B.M.;
RT   "Molecular cloning and characterization of tumor necrosis factor alpha
RT   (TNF-alpha) from the Australian common brushtail possum, Trichosurus
RT   vulpecula.";
RL   Immunol. Cell Biol. 74:151-158(1996).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S83283; AAB49506.1; -; mRNA.
DR   EMBL; AF016102; AAC48766.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT                                /FTId=PRO_0000034457.
FT   CHAIN       ?78    233       Tumor necrosis factor, soluble form.
FT                                /FTId=PRO_0000034458.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (Potential).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25705 MW;  56FDD9F46DC4406E CRC64;

  Query Match             55.7%;  Score 438;  DB 1;  Length 233;
  Best Local Similarity   53.9%;  Pred. No. 1.6e-33;
  Matches   83;  Conservative   28;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          4 SSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
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                 | :  | :||||::|:  ||||| |:   || || ||:|| |||||:|| ||||:|||:|
Db         80 SLQNESAKPVAHLIADQLAEGQLLWVGDVANTLLMNGMELVDNQLVLPSTGLYLVYSQLL 139

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
                ::|  |    ::||| |||  :||| :| ||: |:| |::   :  | : ||||:|| ||
Db        140 YKGSQCGKESLVLTHKISRFTLSYQKKVTLLANIRSSCRKAAEDDGEPSAWYEPVYLAGV 199

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                ||| :||:|  : | |: ||||| ||:||| |||
Db        200 FQLTEGDKLVVDTNYPENLDFAEPGQLYFGAIAL 233


RESULT 75
Q864Y7_TUPTA
ID   Q864Y7_TUPTA   PRELIMINARY;   PRT;   103 AA.
AC   Q864Y7;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Tupaia tana (Large tree shrew).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaia.
OX   NCBI_TaxID=70687;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550769; CAD80056.1; -; Genomic_DNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q864Y7; 1-103.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002223; Prot_inh_Kunz-m.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; UNKNOWN_1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     103    103
SQ   SEQUENCE   103 AA;  11252 MW;  931F85E8B9D95CF3 CRC64;

  Query Match             55.5%;  Score 436;  DB 2;  Length 103;
  Best Local Similarity   80.6%;  Pred. No. 8.1e-34;
  Matches   83;  Conservative   10;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         47 QLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP 106
              ||||||:|||||||||||:| ||||| || ||||| |||||  :|||||||:||||:|:
Db          1 QLVVPSDGLYLIYSQVLFTGLGCPSTPVLFTHTISCIAVSYNNKVNLLSAIKSPCQKESA 60

Qy        107 EGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              |||||:||||||| |||||::|||||||:| | |||||||||
Db         61 EGAEAKPWYEPIYQGGVFQLQKGDRLSAEVNLPHYLDFAESGQ 103


RESULT 76
Q80Z05_DIPME
ID   Q80Z05_DIPME   PRELIMINARY;   PRT;   102 AA.
AC   Q80Z05;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=tnfa;
OS   Dipodomys merriami (Merriam's kangaroo rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Heteromyidae; Dipodomyinae; Dipodomys.
OX   NCBI_TaxID=94247;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22761270; PubMed=12878469; DOI=10.1016/S1055-7903(03)00116-7;
RA   de Jong W.W., van Dijk M.A.M., Poux C., Kappe G., van Rheede T.,
RA   Madsen O.;
RT   "Indels in protein-coding sequences of Euarchontoglires constrain the
RT   rooting of the eutherian tree.";
RL   Mol. Phylogenet. Evol. 28:328-340(2003).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ550771; CAD80058.1; -; Genomic_DNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q80Z05; 2-102.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     102    102
SQ   SEQUENCE   102 AA;  11345 MW;  0640931E1009151A CRC64;

  Query Match             51.5%;  Score 404.5;  DB 2;  Length 102;
  Best Local Similarity   73.5%;  Pred. No. 8.6e-31;
  Matches   75;  Conservative   14;  Mismatches   12;  Indels    1;  Gaps    1;

Qy         48 LVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPE 107
              ||||| |||||:||||||:|:||| |: ::||||: | | ||  :|||||||:||||:| ||
Db          2 LVVPSNGLYLVYSQVLFKGRGC-SSFLVLTHTVGRFATSYPEKVNLLSAIKSPCQKEIPE 60

Qy        108 GAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQ 149
              | | :|||||||||||||:|||||||:| | ||||||:||
Db         61 GPELKPWYEPIYLGGVFQLEKGDRLSAEVNLPQYLDFAEAGQ 102


RESULT 77
Q7YSE3_SHEEP
ID   Q7YSE3_SHEEP   PRELIMINARY;   PRT;    70 AA.
AC   Q7YSE3;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Tumor necrosis factor-alpha (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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OC   Pecora; Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Steele B., Daniel J.A., Sartin J.L.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY289202; AAP43688.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q7YSE3; 1-70.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   70 AA;  7860 MW;  FBECE6F7C3EC916E CRC64;

  Query Match             39.9%;  Score 314;  DB 2;  Length 70;
  Best Local Similarity   84.3%;  Pred. No. 2.7e-22;
  Matches   59;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         88 QTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAES 147
              ||:||:||||:||| ||| ||||||:||||||| |||||||:||||||||| |:|||:|||
Db          1 QTKVNILSAIKSPCHRETLEGAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPEYLDYAES 60

Qy        148 GQVYFGIIAL 157
              ||||||||||
Db         61 GQVYFGIIAL 70


RESULT 78
Q9R136_MERUN
ID   Q9R136_MERUN   PRELIMINARY;   PRT;   101 AA.
AC   Q9R136;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   Tumor necrosis factor (Fragment).
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Gerbillinae; Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Renal lymph node;
RA   Rao U.R., Klei T.R.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF171082; AAD51322.1; -; mRNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q9R136; 40-101.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     101    101
SQ   SEQUENCE   101 AA;  11169 MW;  06B5AF2CAEB62C6C CRC64;

  Query Match             37.0%;  Score 291;  DB 2;  Length 101;
  Best Local Similarity   78.6%;  Pred. No. 7.2e-20;
  Matches   55;  Conservative    9;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  ||:|||||| | | | ||:||:||||||||||:||||||||||:||||:||
Db         32 LRSSSQNASDKPVAHVVPNHQVEEQLEWLSRRANALLANGMELRDNQLVVPSDGLYLVYS 91

Qy         61 QVLFXGQGCP 70
              ||||:|||||
Db         92 QVLFKGQGCP 101


RESULT 79
Q75T06_RABIT
ID   Q75T06_RABIT   PRELIMINARY;   PRT;   70 AA.
AC   Q75T06;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNFa;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Murata T.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB128153; BAD04916.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q75T06; 12-70.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER      70     70
SQ   SEQUENCE   70 AA;  7609 MW;  93BCE5CC41E0F9A4 CRC64;

  Query Match             34.9%;  Score 274;  DB 2;  Length 70;
  Best Local Similarity   77.6%;  Pred. No. 1.9e-18;
  Matches   52;  Conservative   11;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
```

```
              :||:||  ||:|:|||||||| |||||||::|||||||::| |||||||::|||||||
Db          4 LRSASRALSDEPLAHVVANPQVEGQLQWLSQRANALLANGMKLTDNQLVVPADGLYLIYS 63

Qy         61 QVLFXGQ 67
              ||||:||
Db         64 QVLFSGQ 70


RESULT 80
Q2HZD0_PHOSU
ID   Q2HZD0_PHOSU   PRELIMINARY;   PRT;   175 AA.
AC   Q2HZD0;
DT   07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT   07-MAR-2006, sequence version 1.
DT   07-MAR-2006, entry version 1.
DE   Tumor necrosis factor (Fragment).
GN   Name=TNF;
OS   Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Phodopus.
OX   NCBI_TaxID=10044;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15749332;
RA   Pyter L.M., Samuelsson A.R., Quan N., Nelson R.J.;
RT   "Photoperiod alters hypothalamic cytokine gene expression and sickness
RT   responses following immune challenge in female Siberian hamsters
RT   (Phodopus sungorus).";
RL   Neuroscience 131:779-784(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15967631; DOI=10.1016/j.bbi.2005.05.001;
RA   Weil Z.M., Bowers S.L., Pyter L.M., Nelson R.J.;
RT   "Social interactions alter proinflammatory cytokine gene expression
RT   and behavior following endotoxin administration.";
RL   Brain Behav. Immun. 20:72-79(2006).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ358743; ABC88246.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     175    175
SQ   SEQUENCE   175 AA;  19111 MW;  F554FB394AB7413E CRC64;

  Query Match             34.5%;  Score 271.5;  DB 2;  Length 175;
  Best Local Similarity   49.2%;  Pred. No. 1.1e-17;
  Matches   58;  Conservative   14;  Mismatches    7;  Indels   39;  Gaps    2;

Qy           1 VRSSSRTPSDXPVAHVVANPQAEGQLQWL-------------------NRRANALLANG 40
               :||||:  ||:|||||||| | | ||:||                    :||||||||||
Db          50 LRSSSQNSSDKPVAHVVANNQMEEQLEWLSQRANALLANGMSLKDNQLVSRRANALLANG 109

Qy          41 VELRDNQLVVPSEGLYLIYSQVLFXGQGC-------------------PSTHVLLTHT 79
               ::|:|||||:|::||||:||||||:|||                   | :||||||
Db         110 MDLKDNQLVIPADGLYLVYSQVLFKGQGCLPADGLYLVYSQVLFKGQGCSNYVLLTHT 167


RESULT 81
Q95N81_CANFA
ID   Q95N81_CANFA   PRELIMINARY;   PRT;    65 AA.
AC   Q95N81;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Tumor necrosis factor alpha (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fonfara S., Groene A., Koenig M., Wolfgang B.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF349537; AAK54071.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q95N81; 6-65.
DR   Ensembl; ENSCAFG00000000517; Canis familiaris.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 2.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER      65     65
SQ   SEQUENCE   65 AA;  7067 MW;  917C467A05F42B5B CRC64;

  Query Match             34.1%;  Score 268;  DB 2;  Length 65;
  Best Local Similarity   87.7%;  Pred. No. 6.5e-18;
  Matches   57;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          32 RANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXV 91
               |||| ||||||| |||||:|||:||||||||||||:||| |||||||||||||| ||||||:|
Db           1 RANAXLANGVELTDNQLIVPSDGLYLIYSQVLFKGQGXPSTHVLLTHTISRFAVSYQTKV 60

Qy          92 NLLSA 96
               |||||
Db          61 NLLSA 65


RESULT 82
TNFB_MARMO
ID   TNFB_MARMO     STANDARD;      PRT;   205 AA.
AC   Q9JM09; Q9JM12;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 27.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Sciuridae; Xerinae; Marmotini; Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   MEDLINE=20184748; PubMed=10721723; DOI=10.1016/S0378-1119(99)00494-1;
RA   Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
RT   "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
RT   structure, characterization and biological activity.";
RL   Gene 242:295-305(2000).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ----------------------------------------------------------------------
DR   EMBL; AF096268; AAF34868.1; -; Genomic_DNA.
DR   EMBL; AF095586; AAF34864.1; -; mRNA.
DR   HSSP; P01374; 1TNR.
DR   SMR; Q9JM09; 62-205.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     34       By similarity.
FT   CHAIN        35    205      Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034466.
FT   CARBOHYD     96    96       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     46    46       R -> W (in Ref. 1; AAF34864).
SQ   SEQUENCE   205 AA;  22229 MW;  EE1F8D8E4C04C8A7 CRC64;

  Query Match             33.8%;  Score 265.5;  DB 1;  Length 205;
  Best Local Similarity   39.1%;  Pred. No. 5.2e-17;
  Matches   59;  Conservative   26;  Mismatches   55;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP 70
              :| ||:| :|  :  |:|      | | :|  | :| |:||: ||| :||||:|:|:||
Db         62 KPAAHLVGDPSMQNSLRWRANTDRAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGEGCS 121

Qy         71 ----STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                 || : | | :   :  |  :| |||| :| |    |:|    ||   :| | || |
Db        122 SKAVSTPLYLAHEVQLFSSQYPFHVPLLSAQKSVC--PGPQG----PWVRSVYQGAVFLL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :| |: |  |:||  ||
Db        176 TRGDQLSTHTDGISHLLFSPS-SVFFGAFAL 205


RESULT 83
Q7T194_ACASC
ID   Q7T194_ACASC   PRELIMINARY;   PRT;   253 AA.
AC   Q7T194;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Tumor necrosis factor a.
OS   Acanthopagrus schlegeli (Black porgy).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sparidae; Acanthopagrus.
OX   NCBI_TaxID=72011;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Cai Z., Song L., Gao C., Xiang J., Qiu L.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AY335443; AAP94278.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   253 AA;  28003 MW;  A682CB9AABC67867 CRC64;

  Query Match             33.6%;  Score 264;  DB 2;  Length 253;
  Best Local Similarity   39.4%;  Pred. No. 9.7e-17;
  Matches   56;  Conservative   26;  Mismatches   50;  Indels   10;  Gaps    3;

Qy         25 QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF-------XGQGCPSTHVLLT 77
              |::| | :  |    |  | ||::|:|  ||| :|||  |       : :|      |:
Db        113 QVEWKNGQGQAFAQGGFRLVDNKIVIPQTGLYFVYSQASFRVSCSDGDEEGAGRHLTPLS 172

Qy         78 HTISRIAVSYQTXVNLLSAIXSPCQRETPEG--AEAXPWYEPIYLGGVFQLEXGDRLSAE 135
              ||||| : |  |:|:|:||::| ||    |   :: : ||  |||| |||| :|||| |
Db        173 HTISRYSESMGTDVSLMSAVRSACQNTAHEDSYSDGRGWYNTIYLGAVFQLNRGDRLETE 232

Qy        136 INRPDYLDFAESGQVYFGIIAL 157
               |:  |:  : |: :||: ||
Db        233 TNQLSELE-TDEGKTFFGVFAL 253


RESULT 84
TNFB_RABIT
ID   TNFB_RABIT     STANDARD;      PRT;   197 AA.
AC   P10154;
DT   01-JUL-1989, integrated into UniProtKB/Swiss-Prot.
DT   01-AUG-1991, sequence version 2.
DT   07-FEB-2006, entry version 47.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=91065534; PubMed=2249779; DOI=10.1016/0378-1119(90)90364-W;
RA   Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA   Nedospasov S.A.;
RT   "Structural analysis of the rabbit TNF locus, containing the genes
RT   encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT   factor).";
RL   Gene 95:215-221(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=90220566; PubMed=2633043;
RA   Shakhov A.N., Kuprash D.V., Turetskaya R.L., Azizov M.M.,
RA   Andreyeva A.V., Nedospasov S.A.;
RT   "Cloning and structural analysis of genes coding for tumor necrosis
RT   factor and lymphotoxin in rabbits.";
RL   Mol. Biol. (Mosk.) 23:1743-1750(1989).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X55745; CAA39275.1; ALT_SEQ; Genomic_DNA.
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DR   EMBL; M60340; AAA31483.1; -; Genomic_DNA.
DR   EMBL; M60341; AAA31485.1; -; Genomic_DNA.
DR   PIR; JH0309; JH0309.
DR   HSSP; P01374; 1TNR.
DR   SMR; P10154; 54-197.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     26
FT   CHAIN       27    197       Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034470.
FT   CARBOHYD     88     88       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   197 AA;  21126 MW;  0CF18CC90B5E2345 CRC64;

  Query Match             33.1%;  Score 260.5;  DB 1;  Length 197;
  Best Local Similarity   39.1%;  Pred. No. 1.5e-16;
  Matches   59;  Conservative   25;  Mismatches   56;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP 70
              :| ||:| :| |:  |:|      | | :|  | :| |:||| ||| :||||:|:|:||
Db         54 KPAAHLVGDPSAQDSLRWRANTDRAFLRHGFSLSNNSLLVPSSGLYFVYSQVVFSGEGCS 113

Qy         71 ----STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                  | : | |  :   :  |  :| |||| :| |    |:|    ||   :| | || |
Db        114 PKAVPTPLYLAHEVQLFSSQYSFHVPLLSAQKSVC--PGPQG----PWVRSVYQGAVFLL 167

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        168 TQGDQLSTHTDGIAHLLLSPS-SVFFGAFAL 197


RESULT 85
Q6PWY4_PIG
ID   Q6PWY4_PIG     PRELIMINARY;   PRT;    74 AA.
AC   Q6PWY4;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor alpha (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Uterus during early pregnancy;
RX   PubMed=16365405;
RA   Tayade C., Black G.P., Fang Y., Croy B.A.;
RT   "Differential Gene Expression in Endometrium, Endometrial Lymphocytes,
RT   and Trophoblasts during Successful and Abortive Embryo Implantation.";
RL   J. Immunol. 176:148-156(2006).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY572787; AAS78983.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   SMR; Q6PWY4; 11-74.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER      74     74
SQ   SEQUENCE   74 AA;  7995 MW;  A9DAD38B1F1D9E3E CRC64;

  Query Match             33.0%;  Score 259;  DB 2;  Length 74;
  Best Local Similarity   78.1%;  Pred. No. 5.7e-17;
  Matches   50;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         18 ANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTHVLLT 77
              || :||||||| :  |||||||||:|:|||||||::||||||||||:|||||||:| |
Db         11 ANVKAEGQLQWQSGYANALLANGVKLKDNQLVVPTDGLYLIYSQVLFRGQGCPSTNVFLI 70

Qy         78 HTIS 81
              ||||
Db         71 HTIS 74


RESULT 86
Q7T1U4_PAGMA
ID   Q7T1U4_PAGMA   PRELIMINARY;   PRT;   222 AA.
AC   Q7T1U4;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor a.
OS   Pagrus major (Red sea bream) (Chrysophrys major).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sparidae; Pagrus.
OX   NCBI_TaxID=143350;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Cai Z., Song L., Gao C., Qiu L., Xiang J.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY314010; AAP76392.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   222 AA;  24382 MW;  8D8496F855AAF552 CRC64;

  Query Match             32.4%;  Score 255;  DB 2;  Length 222;
  Best Local Similarity   37.2%;  Pred. No. 6e-16;
  Matches   54;  Conservative   29;  Mismatches   52;  Indels   10;  Gaps    3;

Qy         22 AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF-------XGQGCPSTHV 74
              :: |: | : :  |    |  | ||::|:|  ||| :|||  |       : :|    |
Db         79 SKDQVGWKSGQGQAFAQGGFRLVDNKIVIPQTGLYFVYSQASFRVSCSDGEEEGAGGHHT 138
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Qy         75 LLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEG--AEAXPWYEPIYLGGVFQLEXGDRL 132
              |:| ||| : |  ::|:|:||::| ||    :   :: : ||  |||| |||| :||||
Db        139 PLSHRISRSSESMGSDVSLMSAVRSACQNTAQDDSYSDGRGWYNTIYLGAVFQLNRGDRL 198

Qy        133 SAEINRPDYLDFAESGQVYFGIIAL 157
                | |:   |:  | |: :||: ||
Db        199 WTETNQLSELE-TEEGKTFFGVFAL 222


RESULT 87
TNFB_BOVIN
ID   TNFB_BOVIN     STANDARD;      PRT;   204 AA.
AC   Q06600;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 1.
DT   07-FEB-2006, entry version 37.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=94083525; PubMed=8260599; DOI=10.1016/1043-4666(93)90065-D;
RA   Cludts I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
RT   "Cloning and characterization of the tandemly arranged bovine
RT   lymphotoxin and tumour necrosis factor-alpha genes.";
RL   Cytokine 5:336-341(1993).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; Z14137; CAA78510.1; -; Genomic_DNA.
DR   PIR; I46046; S24641.
DR   HSSP; P01374; 1TNR.
DR   SMR; Q06600; 61-204.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     33       By similarity.
FT   CHAIN       34    204       Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034461.
FT   CARBOHYD     95     95      N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   204 AA;  22099 MW;  E2A9F0A2CEDB5425 CRC64;

  Query Match             32.3%;  Score 253.5;  DB 1;  Length 204;
  Best Local Similarity   37.7%;  Pred. No. 7.4e-16;
  Matches   57;  Conservative   26;  Mismatches   57;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGC- 69
              :| ||:| :|  :  |:|       | | :|  | :| |:||: ||| :||||:|:|:||
Db         61 KPAAHLVGDPSTQDSLRWRANTDRAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGRGCF 120

Qy         70 ---PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                  | : | |  :   :  |  :| |||| :| |    |:|    ||   :| | || |
Db        121 PRATPTPLYLAHEVQLFSPQYPFHVPLLSAQKSVC--PGPQG----PWVRSVYQGAVFLL 174

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        175 TRGDQLSTHTDGISHLLLSPS-SVFFGAFAL 204


RESULT 88
TNFB_CANFA
ID   TNFB_CANFA     STANDARD;      PRT;   204 AA.
AC   Q5WR07;
DT   26-APR-2005, integrated into UniProtKB/Swiss-Prot.
DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Wagner J.L., Palti Y., DiDario D.D.;
RT   "Genomic map of a portion of the canine MHC class I histocompatibility
RT   complex.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo (By similarity).
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY423389; AAR27884.1; -; Genomic_DNA.
DR   SMR; Q5WR07; 61-204.
DR   Ensembl; ENSCAFG00000000515; Canis familiaris.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     33       By similarity.
FT   CHAIN       34    204       Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034462.
FT   CARBOHYD     95     95      N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   204 AA;  22033 MW;  B1F88591328F80D8 CRC64;

  Query Match             32.3%;  Score 253.5;  DB 1;  Length 204;
  Best Local Similarity   37.1%;  Pred. No. 7.4e-16;
  Matches   56;  Conservative   27;  Mismatches   57;  Indels   11;  Gaps    4;
```

```
Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGC- 69
              :| ||:: :|  :  |:|      | | :|  | :| |:||: ||| :||||:|:|:||
Db         61 KPAAHLIGDPSIQNSLRWRANTDRAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGEGCF 120

Qy         70 ---PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                    | : | | :   :  |  :| |||| :| |    |:|    ||   :| | || |
Db        121 PKATPTPLYLAHEVQLFSSQYPFHVPLLSAQKSVC--PGPQG----PWVRSVYQGAVFLL 174

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        175 TQGDQLSTHTDGISHLLLSPS-SVFFGAFAL 204


RESULT 89
TNFA_SPAAU
ID   TNFA_SPAAU     STANDARD;      PRT;   253 AA.
AC   Q8JFG3;
DT   23-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Tumor necrosis factor (TNF-alpha).
GN   Name=TNF; Synonyms=TNFA;
OS   Sparus aurata (Gilthead sea bream).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sparidae; Sparus.
OX   NCBI_TaxID=8175;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22067731; PubMed=12073149; DOI=10.1007/s00251-002-0451-y;
RA   Garcia-Castillo J., Pelegrin P., Mulero V., Meseguer J.;
RT   "Molecular cloning and expression analysis of tumor necrosis factor
RT   alpha from a marine fish reveal its constitutive expression and
RT   ubiquitous nature.";
RL   Immunogenetics 54:200-207(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFBR
CC       (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ413189; CAC88353.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    253       Tumor necrosis factor.
FT                                /FTId=PRO_0000185485.
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     58    253       Extracellular (Potential).
SQ   SEQUENCE   253 AA;  27978 MW;  730E2A52900B743A CRC64;

  Query Match             31.9%;  Score 251;  DB 1;  Length 253;
  Best Local Similarity   37.3%;  Pred. No. 1.7e-15;
  Matches   53;  Conservative   28;  Mismatches   51;  Indels   10;  Gaps    3;

Qy         25 QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF-------XGQGCPSTHVLLT 77
                |::| | :  |    |  | ||::|:|  ||| :|||  |       : :|       |:
Db        113 QVEWKNGQGQAFAQGGFRLVDNKIVIPHTGLYFVYSQASFRVSCSDGDEEGAGRHLTPLS 172

Qy         78 HTISRIAVSYQTXVNLLSAIXSPCQRETPEG--AEAXPWYEPIYLGGVFQLEXGDRLSAE 135
              | ||| : |  ::|:|:||::| ||    |   :: : ||  |||| |||| :||:|  |
Db        173 HRISRYSESMGSDVSLMSAVRSACQNTAQEDSYSDGRGWYNTIYLGAVFQLNRGDKLETE 232

Qy        136 INRPDYLDFAESGQVYFGIIAL 157
               |:   |:  : |: :||: ||
Db        233 TNQLSELE-TDEGKTFFGVFAL 253


RESULT 90
TNFB_PIG
ID   TNFB_PIG       STANDARD;      PRT;   204 AA.
AC   P26445;
DT   01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT   01-AUG-1992, sequence version 1.
DT   07-FEB-2006, entry version 41.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   TISSUE=Liver;
RX   MEDLINE=91340150; PubMed=1874444; DOI=10.1016/0378-1119(91)90075-M;
RA   Kuhnert P., Wuethrich C., Peterhans E., Pauli U.;
RT   "The porcine tumor necrosis factor-encoding genes: sequence and
RT   comparative analysis.";
RL   Gene 102:171-178(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Large white; TISSUE=Fibroblast;
RX   MEDLINE=21108615; PubMed=11169259;
RX   DOI=10.1034/j.1399-0039.2001.057001055.x;
RA   Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
RA   Renard C.;
RT   "Sequence of the swine major histocompatibility complex region
RT   containing all non-classical class I genes.";
RL   Tissue Antigens 57:55-65(2001).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; X54859; CAA38638.1; -; Genomic_DNA.
DR   EMBL; AJ251914; CAB63853.1; -; Genomic_DNA.
DR   PIR; S17289; S17289.
DR   HSSP; P01374; 1TNR.
DR   SMR; P26445; 61-204.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
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DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     33
FT   CHAIN        34    204       Lymphotoxin-alpha.
FT                                 /FTId=PRO_0000034469.
FT   CARBOHYD      95     95       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   204 AA;  21960 MW;  81263187435E56AC CRC64;

  Query Match             31.7%;  Score 249.5;  DB 1;  Length 204;
  Best Local Similarity   37.7%;  Pred. No. 1.8e-15;
  Matches   57;  Conservative   25;  Mismatches   58;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGC- 69
              :| ||:| :|      |:|      | | :|  | :| |:||: ||| :||||:|:|:||
Db         61 KPAAHLVGDPSTPDSLRWRANTDRAFLRHGFLLSNNSLLVPTSGLYFVYSQVVFSGEGCF 120

Qy         70 ---PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                 | : | |  :   :  | :| |||| :| |    |:|    ||   :| | || |
Db        121 PKATPTPLYLAHEVQLFSSQYPFHVPLLSAQKSVC--PGPQG----PWVRSVYQGAVFLL 174

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        175 TQGDQLSTHTDGTPHLLLSPS-SVFFGAFAL 204


RESULT 91
TNFB_MACEU
ID   TNFB_MACEU     STANDARD;      PRT;   201 AA.
AC   Q9XT48;
DT   01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1999, sequence version 1.
DT   07-FEB-2006, entry version 31.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=20284948; PubMed=10826697;
RA   Harrison G.A., Deane E.M.;
RT   "cDNA cloning of lymphotoxin alpha (LT-alpha) from a marsupial,
RT   Macropus eugenii.";
RL   DNA Seq. 10:399-403(2000).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AF119336; AAD41773.1; -; mRNA.
DR   HSSP; P01374; 1TNR.
DR   SMR; Q9XT48; 59-201.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL        1     27       By similarity.
FT   CHAIN        28    201       Lymphotoxin-alpha.
FT                                 /FTId=PRO_0000034464.
FT   CARBOHYD      93     93       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   201 AA;  21536 MW;  8C4C371CB5091627 CRC64;

  Query Match             31.7%;  Score 249;  DB 1;  Length 201;
  Best Local Similarity   36.0%;  Pred. No. 2e-15;
  Matches   54;  Conservative   25;  Mismatches   61;  Indels   10;  Gaps    3;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP 70
              :| ||:| :|  :  : |      :| | :|  | :| |:||: ||| :||||:|:|  |
Db         59 KPAAHLVGDPSVQDSIHWRANTDHAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGASCS 118

Qy         71 S---THVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
                 | : |:| :   :  || :| |||| :| |          :||   :| | || |
Db        119 EITPTLLYLSHEVLLFSSKYQVHVPLLSAQKSVC------SGTQGPWMRSVYQGAVFLLT 172

Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              :|||||   :   :|       |:||  ||
Db        173 QGDRLSTYTDGVSHL-LQSPSSVFFGAFAL 201


RESULT 92
Q3T4H4_MACEU
ID   Q3T4H4_MACEU   PRELIMINARY;   PRT;   201 AA.
AC   Q3T4H4;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Lymphotoxin alpha.
GN   Name=LTA;
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=16103651; DOI=10.1159/000086379;
RA   Cross J.G., Harrison G.A., Coggill P., Sims S., Beck S., Deakin J.E.,
RA   Graves J.A.;
RT   "Analysis of the genomic region containing the tammar wallaby
RT   (Macropus eugenii) orthologues of MHC class III genes.";
RL   Cytogenet. Genome Res. 111:110-117(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Harrison G.G., Cross J.G., Deakin J.E., Marshall Graves J.A.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AY853666; AAZ99794.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   201 AA;  21536 MW;  8C4C371CB5091627 CRC64;
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  Query Match             31.7%;  Score 249;  DB 2;  Length 201;
  Best Local Similarity   36.0%;  Pred. No. 2e-15;
  Matches   54;  Conservative   25;  Mismatches   61;  Indels   10;  Gaps    3;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP 70
              :| ||:| :|  :  : |     :| | :|  | :| |:||: ||| :||||:|:|  |
Db         59 KPAAHLVGDPSVQDSIHWRANTDHAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGASCS 118

Qy         71 S---THVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
                | : |:| :   :  || :| |||| :| |       :||   :| | || |
Db        119 EITPTLLYLSHEVLLFSSKYQVHVPLLSAQKSVC------SGTQGPWMRSVYQGAVFLLT 172

Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              :|||||   :   :|       |:||  ||
Db        173 QGDRLSTYTDGVSHL-LQSPSSVFFGAFAL 201


RESULT 93
Q6U817_LATJA
ID   Q6U817_LATJA   PRELIMINARY;   PRT;   241 AA.
AC   Q6U817;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Tumor necrosis factor alpha.
OS   Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Moronidae; Lateolabrax.
OX   NCBI_TaxID=8164;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Qiu L., Song L., Wu L., Cai Z., Xu W., Wang L.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY376595; AAR02413.2; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   241 AA;  26702 MW;  2C493CF80651EA2C CRC64;

  Query Match             31.6%;  Score 248;  DB 2;  Length 241;
  Best Local Similarity   38.0%;  Pred. No. 3.1e-15;
  Matches   54;  Conservative   25;  Mismatches   53;  Indels   10;  Gaps    3;

Qy         25 QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF-------XGQGCPSTHVLLT 77
              ||:| | :  |     |  | :||:|:|  ||| :| |  |        : :|       |:
Db        101 QLEWKNGQGQAFAQGGFRLVNNQIVIPQTGLYFVYCQASFRVSCSNGDEEGAGKGLTPLS 160

Qy         78 HTISRIAVSYQTXVNLLSAIXSPCQRETPEGA--EAXPWYEPIYLGGVFQLEXGDRLSAE 135
              | | | : |  :: :|:||::| ||  | | :    : ||  |||| |||| :|||| |
Db        161 HRIWRYSDSIGSKASLVSAVRSACQSTTQEDSYRAGQGWYNTIYLGAVFQLNRGDRLWTE 220

Qy        136 INRPDYLDFAESGQVYFGIIAL 157
               |:|  |:  : |: :||: ||
Db        221 TNQPSELE-TDEGKTFFGVFAL 241


RESULT 94
Q80WE7_PERMA
ID   Q80WE7_PERMA   PRELIMINARY;   PRT;   202 AA.
AC   Q80WE7;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Lymphotoxin alpha.
GN   Name=Lta;
OS   Peromyscus maniculatus (Deer mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Neotominae; Peromyscus.
OX   NCBI_TaxID=10042;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Schountz T., Hucks J., Prescott J.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY251294; AAP13854.1; -; Genomic_DNA.
DR   HSSP; P01374; 1TNR.
DR   SMR; Q80WE7; 59-202.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   202 AA;  21933 MW;  54C121DFCEBCF15E CRC64;

  Query Match             31.1%;  Score 244.5;  DB 2;  Length 202;
  Best Local Similarity   35.8%;  Pred. No. 5.4e-15;
  Matches   54;  Conservative   27;  Mismatches   59;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGC- 69
              :| ||:| :|  :  | |       | | :|  | :| |:||: ||| :||||:|:|: |
Db         59 KPAAHLVGHPSKQNSLLWRANTDRAFLRHGFSLNNNSLLVPASGLYFVYSQVVFSGESCS 118

Qy         70 ---PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                    : | | :  ::  |  :| ||||      |:    | : :||   :| | || |
Db        119 PKATPAPIYLAHEVQLLSSQYPFHVPLLSA-----QKSVYPGLQ-GPWVRSMYQGAVFLL 172

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              :||:||   :   :| |: |  |:||  ||
Db        173 RKGDQLSTHTDGVSHLHFSPS-SVFFGAFAL 202


RESULT 95
Q9IB42_PAROL
ID   Q9IB42_PAROL   PRELIMINARY;   PRT;   225 AA.
AC   Q9IB42;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor.
OS   Paralichthys olivaceus (Japanese flounder).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Paralichthyidae; Paralichthys.
OX   NCBI_TaxID=8255;
```

```
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20491932; PubMed=11035080;
RA   Hirono I., Nam B., Kurobe T., Aoki T.;
RT   "Molecular cloning, characterization, and expression of TNF cDNA and
RT   gene from Japanese flounder Paralychthys olivaceus.";
RL   J. Immunol. 165:4423-4427(2000).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB040448; BAA94969.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   225 AA;  24965 MW;  8F947FB25FC82658 CRC64;

  Query Match             31.0%;  Score 243.5;  DB 2;  Length 225;
  Best Local Similarity   35.8%;  Pred. No. 7.8e-15;
  Matches   53;  Conservative   27;  Mismatches   55;  Indels   13;  Gaps    4;

Qy         22 AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF----------XGQGCPS 71
              :| :| | |     |    | || || :::|  ||| :|||  |           :|:
Db         79 SENKLVWKNDEGLAFTQGGFELVDNHIIIPRSGLYFVYSQASFRVSCSSDDADDGKEAAE 138

Qy         72 THVL-LTHTISRIAVSYQTXVNLLSAIXSPCQRETPEG-AEAXPWYEPIYLGGVFQLEXG 129
                |:  ::| :      |  |:|:|:||::| ||:   :   : : ||  |||| |||| :|
Db        139 KHLTSISHRVWLFTESLGTQVSLMSAVRSACQKSQEDAYRDGQGWYNAIYLGAVFQLNEG 198

Qy        130 DRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |:|  | |    |:  |||: :||: ||
Db        199 DKLWTETNMLSELE-TESGKTFFGVFAL 225


RESULT 96
Q4W8A0_FUGRU
ID   Q4W8A0_FUGRU   PRELIMINARY;   PRT;   250 AA.
AC   Q4W8A0;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Tumor necrosis factor alpha.
GN   Name=TNF alpha;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15759114; DOI=10.1007/s00251-005-0768-4;
RA   Savan R., Kono R., Igawa D., Sakai M.;
RT   "A novel tumor necrosis factor (TNF) gene present in tandem with
RT   theTNF-alpha gene on the same chromosome in teleosts.";
RL   Immunogenetics 57:140-150(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Ram S., Sakai M.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB183465; BAD98728.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   250 AA;  27708 MW;  71754470CA3188B4 CRC64;

  Query Match             31.0%;  Score 243.5;  DB 2;  Length 250;
  Best Local Similarity   35.3%;  Pred. No. 9e-15;
  Matches   59;  Conservative   32;  Mismatches   61;  Indels   15;  Gaps    6;

Qy          5 SRTPSDXPVAHVVANPQAEG-----QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              ||  | :  |  :      ||      |::| | :  |       :| :| :::|  ||| :|
Db         85 SRISSKAKAAIHLEGSFDEGENRKDQVEWKNGQGQAFAQGDFQLDNNTIIIPKTGLYFVY 144

Qy         60 SQVLF---XGQG---CP-STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEG--AE 110
              ||  |   :|:|     |  :|: |:| : | : |  |:  ||:|::| ||    ||  :|
Db        145 SQASFRVTCGEGDKHSPGKSHIPLSHRVWRYSDSIGTETTLLNAVRSACQNSALEGGYSE 204

Qy        111 AXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                :  | |||| ||||::||:|  | |:   |:  | |: :||: ||
Db        205 GQSCYNAIYLGAVFQLKMGDKLRTETNQLSELE-TEEGKTFFGVFAL 250


RESULT 97
TNFB_RAT
ID   TNFB_RAT       STANDARD;      PRT;   202 AA.
AC   Q06332;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 1.
DT   07-FEB-2006, entry version 41.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=Lta; Synonyms=Tnfb, Tnfsf1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Testis;
RX   MEDLINE=94040766; PubMed=8224868; DOI=10.1016/0378-1119(93)90200-M;
RA   Kwon J., Chung I.Y., Benveniste E.N.;
RT   "Cloning and sequence analysis of the rat tumor necrosis factor-
RT   encoding genes.";
RL   Gene 132:227-236(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Brown Norway;
RX   PubMed=15060004; DOI=10.1101/gr.1987704;
RA   Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA   Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
RT   "The genomic sequence and comparative analysis of the rat major
RT   histocompatibility complex.";
RL   Genome Res. 14:631-639(2004).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
```

```
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; L00981; AAA16276.1; -; Unassigned_DNA.
DR   EMBL; BX883046; CAE84004.1; -; Genomic_DNA.
DR   PIR; JN0869; JN0869.
DR   HSSP; P01374; 1TNR.
DR   SMR; Q06332; 59-202.
DR   Ensembl; ENSRNOG00000000838; Rattus norvegicus.
DR   RGD; 3020; Lta.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     33       By similarity.
FT   CHAIN       34    202       Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034471.
FT   CARBOHYD     93     93       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   202 AA;  22112 MW;  A56963CE33AE0C08 CRC64;

  Query Match             30.9%;  Score 243;  DB 1;  Length 202;
  Best Local Similarity   34.1%;  Pred. No. 7.5e-15;
  Matches   58;  Conservative   27;  Mismatches   63;  Indels   22;  Gaps    5;

Qy          3 SSSRTPSD----------XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVP 51
              |:|||              :| ||:|  |  :  | |      | | :|  | :| |::|
Db         40 SASRTAHQPPQKHLTHGLLKPAAHLVGYPSKQNSLLWRANTDRAFLRHGFSLNNNSLLIP 99

Qy         52 SEGLYLIYSQVLFXGQGCP----STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPE 107
              : ||| :||||:|:|: |      | : | | :   :  |  :| ||||     |:
Db        100 TSGLYFVYSQVVFSGESCSPRAIPTPIYLAHEVQLFSSQYPFHVPLLSA-----QKSVYP 154

Qy        108 GAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              | : :||   :| | || | :||:||   :   :| |: |  |:||  ||
Db        155 GLQ-GPWVRSMYQGAVFLLSKGDQLSTHTDGISHLHFSPS-TVFFGAFAL 202


RESULT 98
Q9IB41_PAROL
ID   Q9IB41_PAROL   PRELIMINARY;   PRT;   225 AA.
AC   Q9IB41;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor.
OS   Paralichthys olivaceus (Japanese flounder).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Paralichthyidae; Paralichthys.
OX   NCBI_TaxID=8255;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20491932; PubMed=11035080;
RA   Hirono I., Nam B., Kurobe T., Aoki T.;
RT   "Molecular cloning, characterization, and expression of TNF cDNA and
RT   gene from Japanese flounder Paralychthys olivaceus.";
RL   J. Immunol. 165:4423-4427(2000).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB040449; BAA94970.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   225 AA;  24889 MW;  7E347FA253BF3643 CRC64;

  Query Match             30.7%;  Score 241.5;  DB 2;  Length 225;
  Best Local Similarity   35.8%;  Pred. No. 1.2e-14;
  Matches   53;  Conservative   27;  Mismatches   55;  Indels   13;  Gaps    4;

Qy         22 AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF----------XGQGCPS 71
              :| :| | |     |    | || || :::|  ||| :|||  |          :|:
Db         79 SENKLVWKNDEGLAFTQGGFELVDNHIIIPRSGLYSVYSQASFRVSCSSDDADDGKEAAE 138

Qy         72 THVL-LTHTISRIAVSYQTXVNLLSAIXSPCQRETPEG-AEAXPWYEPIYLGGVFQLEXG 129
                |:  ::| :      |  |:|:|:||::| ||:   :   : : ||  |||| |||| :|
Db        139 KHLTSISHRVWLFTESLGTQVSLMSAVRSACQKSQEDAYRDGQGWYNAIYLGAVFQLNEG 198

Qy        130 DRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |:|  | |    |:  |||: :||: ||
Db        199 DKLWTETNMLSELE-TESGKTFFGVFAL 225


RESULT 99
TNFB_MOUSE
ID   TNFB_MOUSE     STANDARD;      PRT;   202 AA.
AC   P09225;
DT   01-JUL-1989, integrated into UniProtKB/Swiss-Prot.
DT   01-JUL-1989, sequence version 1.
DT   07-FEB-2006, entry version 49.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=Lta; Synonyms=Tnfb, Tnfsf1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88067722; PubMed=3684584;
RA   Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
RT   "Nucleotide sequence of the murine TNF locus, including the TNF-alpha
RT   (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";
RL   Nucleic Acids Res. 15:9083-9084(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87040736; PubMed=3490653;
RA   Nedospasov S.A., Hirt B., Shakhov A.N., Dobrynin V.N., Kawashima E.,
RA   Accolla R.S., Jongeneel C.V.;
RT   "The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-
RT   beta) are tandemly arranged on chromosome 17 of the mouse.";
RL   Nucleic Acids Res. 14:7713-7725(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87231097; PubMed=3588316;
RA   Gray P.W., Chen E., Tang W.-L., Ruddle N.H.;
RT   "The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.";
RL   Nucleic Acids Res. 15:3937-3937(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87224127; PubMed=2884262;
RA   Li C.B., Gray P.W., Lin P.F., McGrath K.M., Ruddle F.H., Ruddle N.H.;
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RT   "Cloning and expression of murine lymphotoxin cDNA.";
RL   J. Immunol. 138:4496-4501(1987).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87252204; PubMed=2885372;
RA   Gardner S.M., Mock B.A., Hilgers J., Huppi K.E., Roeder W.D.;
RT   "Mouse lymphotoxin and tumor necrosis factor: structural analysis of
RT   the cloned genes, physical linkage, and chromosomal position.";
RL   J. Immunol. 139:476-483(1987).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=129;
RX   PubMed=14656967; DOI=10.1101/gr.1736803;
RA   Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA   Campbell R.D., Hood L.;
RT   "Analysis of the gene-dense major histocompatibility complex class III
RT   region and its comparison to mouse.";
RL   Genome Res. 13:2621-2636(2003).
RN   [7]
RP   NUCLEOTIDE SEQUENCE OF 6-202.
RX   MEDLINE=89144562; PubMed=3147435;
RA   Weil D., Dautry F.;
RT   "Induction of tumor necrosis factor-alpha and -beta and interferon-
RT   gamma mRNA by interleukin 2 in murine lymphocytic cell lines.";
RL   Oncogene Res. 3:409-414(1988).
RN   [8]
RP   NUCLEOTIDE SEQUENCE OF 56-76.
RX   MEDLINE=91042516; PubMed=1700275;
RA   Weil D., Brosset S., Dautry F.;
RT   "RNA processing is a limiting step for murine tumor necrosis factor
RT   beta expression in response to interleukin-2.";
RL   Mol. Cell. Biol. 10:5865-5875(1990).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U06950; AAA18593.1; -; Unassigned_DNA.
DR   EMBL; Y00467; CAA68529.1; -; Genomic_DNA.
DR   EMBL; X06217; CAA29566.1; -; Genomic_DNA.
DR   EMBL; X06218; CAA29567.1; -; Genomic_DNA.
DR   EMBL; Y00137; CAA68330.1; -; Genomic_DNA.
DR   EMBL; M16819; AAA40460.1; -; mRNA.
DR   EMBL; M17015; AAA39450.1; -; Genomic_DNA.
DR   EMBL; AF109719; AAC82485.1; -; Genomic_DNA.
DR   EMBL; X14800; CAA32906.1; -; mRNA.
DR   EMBL; M60586; AAA40461.1; -; Genomic_DNA.
DR   PIR; B27303; B27303.
DR   HSSP; P01374; 1TNR.
DR   SMR; P09225; 59-202.
DR   Ensembl; ENSMUSG00000024402; Mus musculus.
DR   MGI; MGI:104797; Lta.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0006968; P:cellular defense response; TAS.
DR   GO; GO:0006959; P:humoral immune response; IMP.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0048535; P:lymph node development; IMP.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   GO; GO:0006927; P:programmed cell death, transformed cells; TAS.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     33
FT   CHAIN       34    202       Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034467.
FT   CARBOHYD     93     93       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     26     26       A -> P (in Ref. 5).
FT   CONFLICT    161    162       VR -> CG (in Ref. 2).
SQ   SEQUENCE   202 AA;  21999 MW;  F496F83C685950D3 CRC64;

  Query Match             30.6%;  Score 240.5;  DB 1;  Length 202;
  Best Local Similarity   35.8%;  Pred. No. 1.3e-14;
  Matches   54;  Conservative   26;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP 70
              :| ||:|  |  :  | |       | | :|  | :| |::|: ||| :||||:|:|: |
Db         59 KPAAHLVGYPSKQNSLLWRASTDRAFLRHGFSLSNNSLLIPTSGLYFVYSQVVFSGESCS 118

Qy         71 ----STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                  | : | | :   :  | :| ||||     |:    | : :||   :| | || |
Db        119 PRAIPTPIYLAHEVQLFSSQYPFHVPLLSA-----QKSVYPGLQ-GPWVRSMYQGAVFLL 172

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :| |: |  |:||  ||
Db        173 SKGDQLSTHTDGISHLHFSPS-SVFFGAFAL 202


RESULT 100
Q542S2_MOUSE
ID   Q542S2_MOUSE   PRELIMINARY;   PRT;   202 AA.
AC   Q542S2;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A630048P10 product:lymphotoxin A, full insert sequence (Lta
DE   protein) (3 days neonate thymus cDNA, RIKEN full-length enriched
DE   library, clone:A630048P12 product:lymphotoxin A, full insert
DE   sequence).
GN   Name=Lta;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
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RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [10]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid;
RG   NIH MGC Project;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   NUCLEOTIDE SEQUENCE.

  Query Match             30.6%;  Score 240.5;  DB 2;  Length 202;
  Best Local Similarity   35.8%;  Pred. No. 1.3e-14;
  Matches   54;  Conservative   26;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP 70
              :| ||:|  |  :  | |     | | :|  | :| |::|: ||| :||||:|:|: |
Db         59 KPAAHLVGYPSKQNSLLWRASTDRAFLRHGFSLSNNSLLIPTSGLYFVYSQVVFSGESCS 118

Qy         71 ----STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                  | : | | :   :  |  :| ||||     |:    | : :||   :| | || |
Db        119 PRAIPTPIYLAHEVQLFSSQYPFHVPLLSA-----QKSVYPGLQ-GPWVRSMYQGAVFLL 172

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        173 SKGDQLSTHTDGISHLHFSPS-SVFFGAFAL 202


RESULT 101
Q5VJN5_ORENI
ID   Q5VJN5_ORENI   PRELIMINARY;   PRT;   247 AA.
AC   Q5VJN5;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Tumor necrosis factor-alpha.
OS   Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC   Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiini;
OC   Oreochromis.
OX   NCBI_TaxID=8128;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=16199264; DOI=10.1016/j.molimm.2005.01.012;
RA   Praveen K., Evans D.L., Jaso-Friedmann L.;
RT   "Constitutive expression of tumor necrosis factor-alpha in cytotoxic
RT   cells of teleosts and its role in regulation of cell-mediated
RT   cytotoxicity.";
RL   Mol. Immunol. 43:279-291(2006).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY428948; AAR88097.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   247 AA;  27490 MW;  8D4BF0B0F533B2B8 CRC64;

  Query Match             29.8%;  Score 234.5;  DB 2;  Length 247;
  Best Local Similarity   32.9%;  Pred. No. 6.5e-14;
  Matches   53;  Conservative   31;  Mismatches   66;  Indels   11;  Gaps    3;

Qy          6 RTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFX 65
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Db         89 RISSKAKAAIHLEGSDSKGHLEWRNGQGQAFAQGGFKLEANKIIIPHTGLYFVYSQASFR 148

Qy         66 GQGCPSTH---------VLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYE 116
                | :|           :|:| | | : |  ::  |:||::| ||    :    : ||
Db        149 -VICGNTDENEDEEKSLTILSHRIWRYSESMGSSSTLMSALRSACQDTIQDSFSDHGWYN 207

Qy        117 PIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               |||| |||| :|| |  | |:   |:  : |: :||: ||
Db        208 AIYLGAVFQLNEGDTLWTETNQLSELE-TDEGRTFFGVFAL 247


RESULT 102
Q9I970_ONCMY
ID   Q9I970_ONCMY   PRELIMINARY;   PRT;   246 AA.
AC   Q9I970;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor alpha.
GN   Name=tnfa;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Wang T., Laing K.J., Zou J., Holland J., Hirono I., Aoki T.,
RA   Secombes C.J.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ278085; CAB92316.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   246 AA;  27113 MW;  8CD89DBDF867C6CB CRC64;

  Query Match             28.6%;  Score 225;  DB 2;  Length 246;
  Best Local Similarity   36.8%;  Pred. No. 5.3e-13;
  Matches   53;  Conservative   24;  Mismatches   61;  Indels    6;  Gaps    5;

Qy         19 NPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ-GCPSTHVL- 75
              ||      :||      |    | ||: ||:::|  ||: :|||  |: :   |  |
Db        104 NPNLSADTVQWRKDDGQAFSQGGFELQGNQILIPHTGLFFVYSQASFRVKCNSPGEHTTP 163

Qy         76 LTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDRLS 133
              |:| | | : |   : |||| ::| ||:     |    : ||  :||| |||| :||:|
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Db        164 LSHIIWRYSDSIGVNANLLSGVRSVCQQNYGDAESKIGEGWYNAVYLGAVFQLNEGDKLW 223

Qy        134 AEINRPDYLDFAESGQVYFGIIAL 157
                | ||   ::  | |: :||: ||
Db        224 TETNRLTDVE-PEQGKNFFGVFAL 246


RESULT 103
Q9I976_ONCMY
ID   Q9I976_ONCMY   PRELIMINARY;   PRT;   246 AA.
AC   Q9I976;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   Putative tumour necrosis factor alpha.
GN   Name=TNF-alpha;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21153236; PubMed=11231283;
RA   Laing K.J., Wang T., Zou J., Holland J., Hong S., Bols N., Hirono I.,
RA   Aoki T., Secombes C.J.;
RT   "Cloning and expression analysis of rainbow trout Oncorhynchus mykiss
RT   tumour necrosis factor-alpha.";
RL   Eur. J. Biochem. 268:1315-1322(2001).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ277604; CAB89521.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   CHAIN        86    246       putative tumour necrosis factor alpha.
SQ   SEQUENCE   246 AA;  27113 MW;  DCD8971DF867C6C6 CRC64;

  Query Match             28.6%;  Score 225;  DB 2;  Length 246;
  Best Local Similarity   36.8%;  Pred. No. 5.3e-13;
  Matches   53;  Conservative   24;  Mismatches   61;  Indels    6;  Gaps    5;

Qy         19 NPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ-GCPSTHVL- 75
              ||       :||       |    | ||: ||:::|  ||: :|||  |: :   |  |
Db        104 NPNLSADTVQWRKDDGQAFSQGGFELQGNQILIPHTGLFFVYSQASFRVKCNSPGEHTTP 163

Qy         76 LTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDRLS 133
              |:| | | : |   : |||| ::| ||:     |    : ||  :||| |||| :||:|
Db        164 LSHIIWRYSDSIGVNANLLSGVRSVCQQNYGDAESEIGEGWYNAVYLGAVFQLNEGDKLW 223

Qy        134 AEINRPDYLDFAESGQVYFGIIAL 157
                | ||   ::  | |: :||: ||
Db        224 TETNRLTDVE-PEQGKNFFGVFAL 246


RESULT 104
Q5BMN1_SALSA
ID   Q5BMN1_SALSA   PRELIMINARY;   PRT;   188 AA.
AC   Q5BMN1;
DT   12-APR-2005, integrated into UniProtKB/TrEMBL.
DT   12-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Tumor necrosis factor alpha-1 (Fragment).
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Morrison R.N., Zou J., Nowak B.F., Secombes C.J.;
RT   "Cloning and expression of two isoforms of Atlantic salmon (Salmo
RT   salar) tumor necrosis factor-alpha.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY929387; AAX24118.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   188 AA;  20915 MW;  35055E978E9BC721 CRC64;

  Query Match             28.2%;  Score 222;  DB 2;  Length 188;
  Best Local Similarity   37.0%;  Pred. No. 7.2e-13;
  Matches   54;  Conservative   23;  Mismatches   59;  Indels   10;  Gaps    5;

Qy         19 NPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF----XGQGCPSTH 73
              ||       :||       |    | ||: ||:::|  ||: :|||  |    :| |  :|
Db         46 NPNLTADTVQWRKDDGQAFSQGGFELQGNQILIPHTGLFFVYSQASFRVKCNGPGENTTP 105

Qy         74 VLLTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDR 131
                |:| | | : |   : |||| ::| |||     |    : ||  :||| |||| :||:
Db        106 --LSHVIWRYSDSIGVNANLLSGVRSVCQRNYGDAESNIGEAWYNAVYLGAVFQLNEGDK 163

Qy        132 LSAEINRPDYLDFAESGQVYFGIIAL 157
                | | ||   ::  | |: :||:  |
Db        164 LWTETNRLTNVE-PEQGKNFFGVFEL 188


RESULT 105
Q5BMN3_SALSA
ID   Q5BMN3_SALSA   PRELIMINARY;   PRT;   246 AA.
AC   Q5BMN3;
DT   12-APR-2005, integrated into UniProtKB/TrEMBL.
DT   12-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Tumor necrosis factor alpha-1.
GN   Name=TNF-alpha-1;
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Morrison R.N., Zou J., Nowak B.F., Secombes C.J.;
RT   "Cloning and expression of two isoforms of Atlantic salmon (Salmo
RT   salar) tumor necrosis factor-alpha.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ----------------------------------------------------------------------
DR   EMBL; AY929385; AAX24116.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   CHAIN        86    246       tumor necrosis factor alpha-1.
SQ   SEQUENCE   246 AA;  27111 MW;  E8D176B0D2C96ABB CRC64;

  Query Match             28.2%;  Score 222;  DB 2;  Length 246;
  Best Local Similarity   37.0%;  Pred. No. 1e-12;
  Matches   54;  Conservative   23;  Mismatches   59;  Indels   10;  Gaps    5;

Qy         19 NPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF----XGQGCPSTH 73
              ||      :||       |     | ||: ||:::|  ||: :|||  |    :| |  :|
Db        104 NPNLTADTVQWRKDDGQAFSQGGFELQGNQILIPHTGLFFVYSQASFRVKCNGPGENTTP 163

Qy         74 VLLTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDR 131
                |:| | | : |   : |||| ::| |||     |    : ||  :||| |||| :||:
Db        164 --LSHVIWRYSDSIGVNANLLSGVRSVCQRNYGDAESNIGEAWYNAVYLGAVFQLNEGDK 221

Qy        132 LSAEINRPDYLDFAESGQVYFGIIAL 157
              | | ||   ::  | |: :||:  |
Db        222 LWTETNRLTNVE-PEQGKNFFGVFEL 246


RESULT 106
TNFB_HUMAN
ID   TNFB_HUMAN     STANDARD;      PRT;   205 AA.
AC   P01374; Q8N4C3; Q9UKS8;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   01-JUL-1989, sequence version 2.
DT   07-FEB-2006, entry version 75.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87217060; PubMed=3555974;
RA   Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
RA   Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
RA   Filippov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,
RA   Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;
RT   "Tandem arrangement of genes coding for tumor necrosis factor (TNF-
RT   alpha) and lymphotoxin (TNF-beta) in the human genome.";
RL   Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86086150; PubMed=3001109;
RA   Nedwin G.E., Jarrett-Nedwin J., Smith D.H., Naylor S.L.,
RA   Sakaguchi A.Y., Goeddel D.V., Gray P.W.;
RT   "Structure and chromosomal localization of the human lymphotoxin
RT   gene.";
RL   J. Cell. Biochem. 29:171-181(1985).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87057135; PubMed=3536896;
RA   Kobayashi Y., Miyamoto D., Asada M., Obinata M., Osawa T.;
RT   "Cloning and expression of human lymphotoxin mRNA derived from a human
RT   T cell hybridoma.";
RL   J. Biochem. 100:727-733(1986).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85086243; PubMed=6334807;
RA   Gray P.W., Aggarwal B.B., Benton C.V., Bringman T.S., Henzel W.J.,
RA   Jarrett J.A., Leung D.W., Moffat B., Ng P., Svedersky L.P.,
RA   Palladino M.A., Nedwin G.E.;
RT   "Cloning and expression of cDNA for human lymphotoxin, a lymphokine
RT   with tumour necrosis activity.";
RL   Nature 312:721-724(1984).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92339500; PubMed=1353024; DOI=10.1016/0014-5793(92)80425-G;
RA   Matsuyama N., Okawa N., Tsukii Y., Endo T., Kaji A.;
RT   "Nucleotide sequence of a cDNA encoding human tumor necrosis factor
RT   beta from B lymphoblastoid cell RPMI 1788.";
RL   FEBS Lett. 302:141-144(1992).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93272029; PubMed=8499947;
RA   Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
RA   Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
RA   Cohen D.;
RT   "Dense Alu clustering and a potential new member of the NF kappa B
RT   family within a 90 kilobase HLA class III segment.";
RL   Nat. Genet. 3:137-145(1993).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99218514; PubMed=10202016;
RA   Neville M.J., Campbell R.D.;
RT   "A new member of the Ig superfamily and a V-ATPase G subunit are among
RT   the predicted products of novel genes close to the TNF locus in the
RT   human MHC.";
RL   J. Immunol. 162:4745-4754(1999).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=14656967; DOI=10.1101/gr.1736803;
RA   Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA   Campbell R.D., Hood L.;
RT   "Analysis of the gene-dense major histocompatibility complex class III
RT   region and its comparison to mouse.";
RL   Genome Res. 13:2621-2636(2003).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Shiina S., Tamiya G., Oka A., Inoko H.;
RT   "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ARG-13; PRO-51 AND
RP   ASN-60.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ARG-13; PRO-51 AND
RP   ASN-60.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [12]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ARG-13.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [13]
RP   PARTIAL PROTEIN SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND VARIANT
RP   ASN-60.
RX   MEDLINE=93083656; PubMed=1451807; DOI=10.1016/0014-5793(92)81467-Z;
RA   Voigt C.G., Maurer-Fogy I., Adolf G.R.;
RT   "Natural human tumor necrosis factor beta (lymphotoxin). Variable O-
RT   glycosylation at Thr7, proteolytic processing, and allelic
RT   variation.";
RL   FEBS Lett. 314:85-88(1992).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=92129275; PubMed=1733919;
RA   Eck M.J., Ultsch M., Rinderknecht E., de Vos A.M., Sprang S.R.;
RT   "The structure of human lymphotoxin (tumor necrosis factor-beta) at
RT   1.9-A resolution.";
RL   J. Biol. Chem. 267:2119-2122(1992).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 61-205 OF COMPLEX WITH
RP   TNFR1.
RX   MEDLINE=93258809; PubMed=8387891; DOI=10.1016/0092-8674(93)90132-A;
RA   Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,
RA   Broger C., Loetscher H., Lesslauer W.;
RT   "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT   beta complex: implications for TNF receptor activation.";
RL   Cell 73:431-445(1993).
RN   [16]
RP   VARIANT ASN-60.
RX   MEDLINE=91086846; PubMed=1670638; DOI=10.1084/jem.173.1.209;
RA   Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA   Riethmueller G., Weiss E.H.;
RT   "Polymorphic structure of the tumor necrosis factor (TNF) locus: an
RT   NcoI polymorphism in the first intron of the human TNF-beta gene
RT   correlates with a variant amino acid in position 26 and a reduced
RT   level of TNF-beta production.";
RL   J. Exp. Med. 173:209-219(1991).
RN   [17]
RP   VARIANT PRO-125.
RX   MEDLINE=91139175; PubMed=1671667; DOI=10.1007/BF00211695;
RA   Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT   "Haplotypic polymorphisms of the TNFB gene.";
RL   Immunogenetics 33:50-53(1991).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits.
CC   -!- INTERACTION:
CC       Q92956:TNFRSF14; NbExp=1; IntAct=EBI-524105, EBI-523409;
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X01393; CAA25649.1; -; mRNA.
DR   EMBL; X02911; CAA26670.1; -; Genomic_DNA.
DR   EMBL; D00102; BAA00064.1; -; mRNA.
DR   EMBL; M16441; AAA61199.1; -; Genomic_DNA.
DR   EMBL; D12614; BAA02139.1; -; mRNA.
DR   EMBL; M55913; AAB59455.1; -; Genomic_DNA.
DR   EMBL; Z15026; CAA78746.1; -; Genomic_DNA.
DR   EMBL; Y14768; CAA75071.1; -; Genomic_DNA.
DR   EMBL; AF129756; AAD18092.1; -; Genomic_DNA.
DR   EMBL; BA000025; BAB63397.1; -; Genomic_DNA.
DR   EMBL; AY070490; AAL49956.1; -; Genomic_DNA.
DR   EMBL; AY216498; AAO21135.1; -; Genomic_DNA.
DR   EMBL; BC034729; AAH34729.1; -; mRNA.
DR   EMBL; A06316; CAA00536.1; -; Unassigned_RNA.
DR   PIR; A92755; QWHUX.
DR   PDB; 1TNR; X-ray; A=62-205.
DR   IntAct; P01374; -.
DR   GlycoSuiteDB; P01374; -.

  Query Match             27.7%;  Score 217.5;  DB 1;  Length 205;
  Best Local Similarity   33.1%;  Pred. No. 2.2e-12;
  Matches   50;  Conservative   30;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQG-- 68
              :| ||:: :|  :  | |      | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                |: : | | :   :  |  :| |||:     |:    | : :||   :| |  |||
Db        122 PKATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        176 TQGDQLSTHTDGIPHLVLSPS-TVFFGAFAL 205


RESULT 107
TNFB_PANTR
ID   TNFB_PANTR     STANDARD;      PRT;   205 AA.
AC   P61125;
DT   10-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT   10-MAY-2004, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=22381002; PubMed=12493009;
RX   DOI=10.1034/j.1600-065X.2002.19008.x;
RA   Kulski J.K., Shiina T., Anzai T., Kohara S., Inoko H.;
RT   "Comparative genomic analysis of the MHC: the evolution of class I
RT   duplication blocks, diversity and complexity from shark to man.";
RL   Immunol. Rev. 190:95-122(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;
RA   Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA   Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA   Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA   Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT   "Comparative sequencing of human and chimpanzee MHC class I regions
RT   unveils insertions/deletions as the major path to genomic
RT   divergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo (By similarity).
```

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CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB054536; BAB83883.1; -; Genomic_DNA.
DR   EMBL; BA000041; BAC78158.1; -; Genomic_DNA.
DR   SMR; P61125; 62-205.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     34       By similarity.
FT   CHAIN       35    205       Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034468.
FT   CARBOHYD     41     41      O-linked; partial (By similarity).
FT   CARBOHYD     96     96      N-linked (GlcNAc. . .) (By similarity).
SQ   SEQUENCE   205 AA;  22350 MW;  E102E1CD53D58A98 CRC64;

  Query Match             27.7%;  Score 217.5;  DB 1;  Length 205;
  Best Local Similarity   33.1%;  Pred. No. 2.2e-12;
  Matches   50;  Conservative   30;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:: :|  :  | |       | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                |: : | | :   :  |  :| |||:     |:    | : :||   :| |  |||
Db        122 PKATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        176 TQGDQLSTHTDGIPHLVLSPS-TVFFGAFAL 205


RESULT 108
Q5STV3_HUMAN
ID   Q5STV3_HUMAN   PRELIMINARY;   PRT;   205 AA.
AC   Q5STV3;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Lymphotoxin alpha (TNF superfamily, member 1).
GN   Name=LTA; ORFNames=DASS-280D8.1-001, XXbac-BPG296P20.9-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
RT   "Genome diversity in HLA: A new strategy for detection of genetic
RT   polymorphisms in expressed genes within the HLA class III and class I
RT   regions.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL662801; CAI18291.1; -; Genomic_DNA.
DR   EMBL; BX248519; CAI41939.1; -; Genomic_DNA.
DR   EMBL; AB088112; BAC54943.1; -; Genomic_DNA.
DR   SMR; Q5STV3; 62-205.
DR   Ensembl; ENSG00000173503; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   205 AA;  22297 MW;  1BBD5E7D496A3A82 CRC64;

  Query Match             27.7%;  Score 217.5;  DB 2;  Length 205;
  Best Local Similarity   33.1%;  Pred. No. 2.2e-12;
  Matches   50;  Conservative   30;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:: :|  :  | |       | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                |: : | | :   :  |  :| |||:     |:    | : :||   :| |  |||
Db        122 PKATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        176 TQGDQLSTHTDGIPHLVLSPS-TVFFGAFAL 205


RESULT 109
Q6FG55_HUMAN
ID   Q6FG55_HUMAN   PRELIMINARY;   PRT;   205 AA.
AC   Q6FG55;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   LTA protein (Lymphotoxin alpha) (TNF superfamily, member 1).
GN   Name=LTA; ORFNames=DAQB-87N14.7-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; CR542253; CAG47049.1; -; mRNA.
DR   EMBL; CR542273; CAG47069.1; -; mRNA.
DR   EMBL; AL929587; CAI18648.1; -; Genomic_DNA.
DR   SMR; Q6FG55; 62-205.
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DR   Ensembl; ENSG00000173503; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   205 AA;  22350 MW;  E102E1CD53D58A98 CRC64;

  Query Match             27.7%;  Score 217.5;  DB 2;  Length 205;
  Best Local Similarity   33.1%;  Pred. No. 2.2e-12;
  Matches   50;  Conservative   30;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:: :|  :  | |       | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                |: : | | :   :  | :| |||:     |:    | : :||   :| |  |||
Db        122 PKATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        176 TQGDQLSTHTDGIPHLVLSPS-TVFFGAFAL 205


RESULT 110
Q5ST95_HUMAN
ID   Q5ST95_HUMAN   PRELIMINARY;   PRT;   205 AA.
AC   Q5ST95;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-MAR-2006, entry version 6.
DE   Lymphotoxin alpha (TNF superfamily, member 1).
GN   Name=LTA; ORFNames=XXbac-BCX270M2.14-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood leukocyte;
RA   Shiina T., Ota M., Takasu M., Katsuyama Y., Hashimoto N., Tokunaga K.,
RA   Inoko H.;
RT   "Genome diversity in HLA: A new strategy for detection of genetic
RT   polymorphisms in expressed genes within the HLA class III and class I
RT   regions.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AL662847; CAI17677.1; -; Genomic_DNA.
DR   EMBL; AB202113; BAE78638.1; -; Genomic_DNA.
DR   SMR; Q5ST95; 62-205.
DR   Ensembl; ENSG00000173503; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   205 AA;  22310 MW;  BA0C25B7930A3A92 CRC64;

  Query Match             27.7%;  Score 217.5;  DB 2;  Length 205;
  Best Local Similarity   33.1%;  Pred. No. 2.2e-12;
  Matches   50;  Conservative   30;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:: :|  :  | |       | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                |: : | | :   :  | :| |||:     |:    | : :||   :| |  |||
Db        122 PKATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :||:||   :   :|  : |  |:||  ||
Db        176 TQGDQLSTHTDGIPHLVLSPS-TVFFGAFAL 205


RESULT 111
TNFB_MACMU
ID   TNFB_MACMU     STANDARD;      PRT;   205 AA.
AC   Q5TM20;
DT   16-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT   21-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE   factor ligand superfamily member 1).
GN   Name=LTA; Synonyms=TNFB, TNFSF1;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15269276; DOI=10.1093/molbev/msh216;
RA   Kulski J.K., Anzai T., Shiina T., Inoko H.;
RT   "Rhesus macaque class I duplicon structures, organization, and
RT   evolution within the alpha block of the major histocompatibility
RT   complex.";
RL   Mol. Biol. Evol. 21:2079-2091(2004).
CC   -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC       TNFRSF1A/TNFR1, TNFRSF1B/TNFBR and TNFRSF14/HVEM. In its
CC       heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC       produced by lymphocytes and cytotoxic for a wide range of tumor
CC       cells in vitro and in vivo.
CC   -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC       LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC       associated (heterotrimers) (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB128049; BAD69725.1; -; Genomic_DNA.
DR   SMR; Q5TM20; 62-205.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
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DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Signal.
FT   SIGNAL       1     34       By similarity.
FT   CHAIN       35    205       Lymphotoxin-alpha.
FT                               /FTId=PRO_0000034465.
FT   CARBOHYD     41     41      O-linked; partial (By similarity).
FT   CARBOHYD     96     96      N-linked (GlcNAc. . .) (By similarity).
SQ   SEQUENCE   205 AA;  22360 MW;  5EE2A7FCE556548A CRC64;

  Query Match             27.5%;  Score 216.5;  DB 1;  Length 205;
  Best Local Similarity   33.1%;  Pred. No. 2.7e-12;
  Matches   50;  Conservative   29;  Mismatches   61;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:: :|  :  | |      | | :|  | :| |:||: |:| :|||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                 | : | | :   :  |  :| |||:     |:    | : :||   :| |  |||
Db        122 PKATPTPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              :||:||   :   :|  : |  |:||  ||
Db        176 TQGDQLSTHTDGIPHLVLSPS-TVFFGAFAL 205


RESULT 112
Q4L212_AOTNA
ID   Q4L212_AOTNA   PRELIMINARY;   PRT;   203 AA.
AC   Q4L212;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   TNF beta (Fragment).
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15271379; DOI=10.1016/j.cyto.2004.04.004;
RA   Pico de Coana Y., Barrero C., Cajiao I., Mosquera C., Patarroyo M.E.,
RA   Patarroyo M.A.;
RT   "Quantifying Aotus monkey cytokines by real-time quantitative RT-
RT   PCR.";
RL   Cytokine 27:129-133(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Rodriguez J.A., Pico de Coana Y., Patarroyo M.A.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY373461; AAR22308.1; -; mRNA.
DR   SMR; Q4L212; 62-203.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER     203    203
SQ   SEQUENCE   203 AA;  22210 MW;  1C275FC68980F637 CRC64;

  Query Match             27.2%;  Score 213.5;  DB 2;  Length 203;
  Best Local Similarity   33.3%;  Pred. No. 5.2e-12;
  Matches   49;  Conservative   30;  Mismatches   57;  Indels   11;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:| :|  :  |:|      | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLVGDPSNQKSLRWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                 | : | | :   :  |  :| |||:     |:    | : :||   :| |  |||
Db        122 PKATPTPLYLAHEVQLFSSQYPFHVSLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFG 153
              :||:||   :   :|  : |  |:||
Db        176 TQGDQLSTHTDGIHHLVLSPS-TVFFG 201


RESULT 113
Q9I8I0_SALFO
ID   Q9I8I0_SALFO   PRELIMINARY;   PRT;   255 AA.
AC   Q9I8I0;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 20.
DE   Tumor necrosis factor.
GN   Name=TNF;
OS   Salvelinus fontinalis (Brook trout) (Brook char).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX   NCBI_TaxID=8038;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Bobe J., Goetz F.W.;
RT   "Molecular cloning and expression of a TNF receptor and two TNF
RT   ligands in the fish ovary.";
RL   Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF276961; AAF86331.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   255 AA;  28006 MW;  7C50501F838FB03D CRC64;

  Query Match             27.1%;  Score 213;  DB 2;  Length 255;
  Best Local Similarity   35.6%;  Pred. No. 7.9e-12;
  Matches   52;  Conservative   25;  Mismatches   59;  Indels   10;  Gaps    5;

Qy         19 NPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF----XGQGCPSTH 73
              ||      :||       |    | :|:|::|  ||: :|||  |    :| |  :|
Db        113 NPNLTADTVQWRKDDGQAFSQGGFKLQGNQILIPHTGLFFVYSQASFRVKCNGPGERTTP 172

Qy         74 VLLTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDR 131
                |:| | | : |   : |||| ::| ||:     |    : ||  :||  |||| :||:
Db        173 --LSHVICRYSDSIGVNANLLSGVRSVCQQNYGNAESNIGEGWYNAVYLSAVFQLNEGDK 230
```

```
Qy        132 LSAEINRPDYLDFAESGQVYFGIIAL 157
              |  | ||   ::  | |: :||: ||
Db        231 LWTETNRLTDVE-PEHGKNFFGVFAL 255


RESULT 114
Q9ERC9_MESAU
ID   Q9ERC9_MESAU   PRELIMINARY;   PRT;   127 AA.
AC   Q9ERC9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Tumor necrosis factor (Fragment).
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Dobrzanska Z., Wieckiewicz J., Bigda J.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF315292; AAG33236.1; -; mRNA.
DR   HSSP; P06804; 2TNF.
DR   SMR; Q9ERC9; 78-127.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     127    127
SQ   SEQUENCE   127 AA;  13870 MW;  74D109C76E25DAF0 CRC64;

  Query Match             27.0%;  Score 212;  DB 2;  Length 127;
  Best Local Similarity   67.2%;  Pred. No. 3.9e-12;
  Matches   39;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLI 58
              :||||:  :|:|||||||| | | ||:||: |||||||||: |:||||||:|::||||:
Db         70 LRSSSQNSNDKPVAHVVANHQVEEQLEWLSHRANALLANGMSLKDNQLVIPADGLYLV 127


RESULT 115
Q8K3Y7_RAT
ID   Q8K3Y7_RAT     PRELIMINARY;   PRT;   252 AA.
AC   Q8K3Y7;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   TNF superfamily ligand TL1A.
GN   Name=Tnfsf15;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=21909416; PubMed=11911831; DOI=10.1016/S1074-7613(02)00283-2;
RA   Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA   Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA   Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA   Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT   "TL1A is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
RT   cell costimulator.";
RL   Immunity 16:479-492(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF520787; AAM77368.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSRNOG00000008930; Rattus norvegicus.
DR   RGD; 628735; Tnfsf15.
DR   GO; GO:0005123; F:death receptor binding; IDA.
DR   GO; GO:0006919; P:caspase activation; IDA.
DR   GO; GO:0050715; P:positive regulation of cytokine secretion; IDA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   252 AA;  28029 MW;  7789E6556D46F293 CRC64;

  Query Match             26.8%;  Score 211;  DB 2;  Length 252;
  Best Local Similarity   30.7%;  Pred. No. 1.2e-11;
  Matches   51;  Conservative   29;  Mismatches   60;  Indels   26;  Gaps    5;

Qy          7 TPS-DXPVAHVVANPQAE--------GQLQWLNRRANALLANGVELRDNQLVVPSEGLYL 57
              ||| |:| ||:    |             | | |    |   | :   :  ||:|  | |
Db         90 TPSRDKPKAHLTIMRQTPVPHLKNELAAALHWENNLGMAFTKNRMNYTNKFLVIPESGDYF 149

Qy         58 IYSQVLFXG--QGC--------PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPE 107
              ||||: |:|    |         |     :|  |:::| ||  : :||:  :| |:
Db        150 IYSQITFRGTTSECGDISRVRRPKKPDSITVVITKVADSYPEPAHLLTGTKSVCE----- 204

Qy        108 GAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
                :: |::||||| :| ||:||||   ::    :|: :  : :||
Db        205 --ISSNWFQPIYLGAMFSLEEGDRLMVNVSDISLVDYTKEDKTFFG 248


RESULT 116
Q9DEP9_ONCMY
ID   Q9DEP9_ONCMY   PRELIMINARY;   PRT;   255 AA.
AC   Q9DEP9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Tumor necrosis factor.
GN   Name=tnf;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Zou J., Laing K.J., Wang T., Secombes C.J.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ401377; CAC16408.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
```

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DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   255 AA;  28175 MW;  45007CB3F7C418C7 CRC64;

  Query Match             26.5%;  Score 208;  DB 2;  Length 255;
  Best Local Similarity   35.6%;  Pred. No. 2.4e-11;
  Matches   52;  Conservative   25;  Mismatches   59;  Indels   10;  Gaps    5;

Qy         19 NPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF----XGQGCPSTH 73
              ||      :||       |    | :|: ||:::|  ||: :||| .|    :| |  :|
Db        113 NPNLTADTVQWRKDDGQAFSQGGFKLQGNQILIPHTGLFFVYSQASFRVKCNGPGERTTP 172

Qy         74 VLLTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDR 131
                 |:| | | : |   : |||| ::| ||:      |    : ||  :||  |||| :||:
Db        173 --LSHVIWRYSDSIGDKGNLLSGVRSVCQQNYGNDESNIGEGWYNAVYLSAVFQLNEGDK 230

Qy        132 LSAEINRPDYLDFAESGQVYFGIIAL 157
              |  | ||   ::  | |: :||: ||
Db        231 LWTETNRLTDVE-PEQGKNFFGVFAL 255


RESULT 117
Q5BMN0_SALSA
ID   Q5BMN0_SALSA   PRELIMINARY;   PRT;   188 AA.
AC   Q5BMN0;
DT   12-APR-2005, integrated into UniProtKB/TrEMBL.
DT   12-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Tumor necrosis factor alpha-2 (Fragment).
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Morrison R.N., Zou J., Nowak B.F., Secombes C.J.;
RT   "Cloning and expression of two isoforms of Atlantic salmon (Salmo
RT   salar) tumor necrosis factor-alpha.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY929388; AAX24119.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   188 AA;  20958 MW;  BBE57A361F98C6F9 CRC64;

  Query Match             26.3%;  Score 207;  DB 2;  Length 188;
  Best Local Similarity   35.2%;  Pred. No. 2e-11;
  Matches   51;  Conservative   25;  Mismatches   61;  Indels    8;  Gaps    5;

Qy         19 NPQ-AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPS---THV 74
              ||      :||       |    | :|: ||:::|  ||: :|||  |: : | |
Db         46 NPNLTANTVQWRKDDGQAFSQGGFKLQGNQILIPHTGLFFVYSQASFRVK-CNSPGERTT 104

Qy         75 LLTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDRL 132
                |:| | | : |   : |||| ::| ||:      |    : ||  :||  |||| :||:|
Db        105 PLSHVIWRYSDSIGDNANLLSGVRSVCQQNYGNSESNIGEGWYNAVYLSAVFQLNEGDKL 164

Qy        133 SAEINRPDYLDFAESGQVYFGIIAL 157
                | ||   ::  | |: :||: ||
Db        165 WTETNRLTEVE-PEQGKNFFGVFAL 188


RESULT 118
Q5BMN2_SALSA
ID   Q5BMN2_SALSA   PRELIMINARY;   PRT;   246 AA.
AC   Q5BMN2;
DT   12-APR-2005, integrated into UniProtKB/TrEMBL.
DT   12-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Tumor necrosis factor alpha-2.
GN   Name=TNF-alpha-2;
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Morrison R.N., Zou J., Nowak B.F., Secombes C.J.;
RT   "Cloning and expression of two isoforms of Atlantic salmon (Salmo
RT   salar) tumor necrosis factor-alpha.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY929386; AAX24117.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   CHAIN        85    246       tumor necrosis factor alpha-2.
SQ   SEQUENCE   246 AA;  27151 MW;  B88BB9BFF84C2CF8 CRC64;

  Query Match             26.3%;  Score 207;  DB 2;  Length 246;
  Best Local Similarity   35.2%;  Pred. No. 2.9e-11;
  Matches   51;  Conservative   25;  Mismatches   61;  Indels    8;  Gaps    5;

Qy         19 NPQ-AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPS---THV 74
              ||      :||       |    | :|: ||:::|  ||: :|||  |: : | |
Db        104 NPNLTANTVQWRKDDGQAFSQGGFKLQGNQILIPHTGLFFVYSQASFRVK-CNSPGERTT 162

Qy         75 LLTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDRL 132
                |:| | | : |   : |||| ::| ||:      |    : ||  :||  |||| :||:|
Db        163 PLSHVIWRYSDSIGDNANLLSGVRSVCQQNYGNSESNIGEGWYNAVYLSAVFQLNEGDKL 222

Qy        133 SAEINRPDYLDFAESGQVYFGIIAL 157
              | ||   ::  | |: :||: ||
Db        223 WTETNRLTEVE-PEQGKNFFGVFAL 246


RESULT 119
Q6T9C7_BRARE
ID   Q6T9C7_BRARE   PRELIMINARY;   PRT;   234 AA.
AC   Q6T9C7;
```

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DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor.
GN   Name=tnfa;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15752547; DOI=10.1016/j.dci.2004.10.007;
RA   Pressley M.E., Phelan P.E., Eckhard Witten P., Mellon M.T., Kim C.H.;
RT   "Pathogenesis and inflammatory response to Edwardsiella tarda
RT   infection in the zebrafish.";
RL   Dev. Comp. Immunol. 29:501-513(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Phelan P.E. III, Mellon M.M., Kim C.H.;
RT   "Identification and Characterization of a Putative Tumor Necrosis
RT   Factor (TNF) sequence in Danio rerio.";
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY427649; AAR06286.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   Ensembl; ENSDARG00000009511; Danio rerio.
DR   ZFIN; ZDB-GENE-050317-1; tnfa.
DR   GO; GO:0005576; C:extracellular region; TAS.
DR   GO; GO:0005125; F:cytokine activity; TAS.
DR   GO; GO:0006955; P:immune response; IDA.
DR   GO; GO:0046685; P:response to arsenic; IDA.
DR   GO; GO:0009615; P:response to virus; IDA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   234 AA;  25826 MW;  6E88DCF46D3F131C CRC64;

  Query Match             25.8%;  Score 203;  DB 2;  Length 234;
  Best Local Similarity   31.3%;  Pred. No. 6.5e-11;
  Matches   51;  Conservative   32;  Mismatches   68;  Indels   12;  Gaps    7;

Qy          2 RSSSRTPSDXPVAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              | |    : :   |:     :| : | | : :  |  : |::| : ::::| :|:| :||
Db         77 RISQGNFTSKAAIHLTGGYNSESKTLDWRDDQDQAFSSGGLKLVNREIIIPDDGIYFVYS 136

Qy         61 QVLFXGQGCPS----THVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYE 116
              ||  :   | |      ||::| : | : ||  :  | |||:| | :| ||      ||
Db        137 QVSLH-ISCTSELTEEQVLMSHAVMRFSESYGGKKPLFSAIRSICTQE-PESENL--WYN 192

Qy        117 PIYLGGVFQLEXGDRLSAEINRPDYLDFAE--SGQVYFGIIAL 157
                ||||  | | :|||| :      |   | :|: :||:  |
Db        193 TIYLGAAFHLREGDRLGTDTTTA-LLPMVENDNGKTFFGVFGL 234


RESULT 120
Q50L61_CHICK
ID   Q50L61_CHICK   PRELIMINARY;   PRT;   239 AA.
AC   Q50L61;
DT   07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   07-JUN-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   TL1A.
GN   Name=ChTL1A;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tetsuya T., Sato K., Takahashi K., Akiba Y.;
RT   "Molecular cloning and identification of chicken TL1A.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Takimoto T., Sato K., Takahashi K., Akiba Y.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB194710; BAD98253.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   239 AA;  26315 MW;  561D007CB8D00575 CRC64;

  Query Match             25.8%;  Score 203;  DB 2;  Length 239;
  Best Local Similarity   28.5%;  Pred. No. 6.7e-11;
  Matches   45;  Conservative   34;  Mismatches   63;  Indels   16;  Gaps    3;

Qy          9 SDXPVAHVVANPQAEGQ--------LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :::| ||:     |              ||| ::|  |    | :    | ||:|  | | :|:
Db         89 AEKPRAHLTVKKQEPSSTTGSHLPILQWEDKRGLAFTKNNLSYSSNALVIPVSGDYYVYA 148

Qy         61 QVLFXGQGCPSTHV-LLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIY 119
              || |:|     |:    :|  |:::  ||  :  ||:: ::  :        | : |::|||
Db        149 QVTFRGPSDTSSKTSSVTAVITKVTDSYPEPTQLLTSTKTLSE-------ERNNWFQPIY 201

Qy        120 LGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              || |  ||:||:|   ::    :|: :  : :||   |
Db        202 LGAVVSLEIGDKLMVNVSDIKLVDYTKEHKTFFGAFLL 239


RESULT 121
Q5HYS4_HUMAN
ID   Q5HYS4_HUMAN   PRELIMINARY;   PRT;   183 AA.
AC   Q5HYS4;
DT   15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT   15-FEB-2005, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Lymphotoxin alpha (TNF superfamily, member 1) (Fragment).
GN   ORFNames=DASS-280D8.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BX248519; CAI41938.1; -; Genomic_DNA.
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DR   SMR; Q5HYS4; 62-183.
DR   Ensembl; ENSG00000173503; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER     183     183
SQ   SEQUENCE   183 AA;  19988 MW;  DC09F2F57CF75F47 CRC64;

  Query Match             25.7%;  Score 202;  DB 2;  Length 183;
  Best Local Similarity   33.9%;  Pred. No. 5.8e-11;
  Matches   43;  Conservative   26;  Mismatches   48;  Indels   10;  Gaps    3;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:: :|  :  | |      | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
                |: : | | :   :  |  :| |||:     |:    | : :||   :| |  |||
Db        122 PKATSSPLYLAHEVQLFSSQYPFHVPLLSS-----QKMVYPGLQ-EPWLHSMYHGAAFQL 175

Qy        127 EXGDRLS 133
               :||:||
Db        176 TQGDQLS 182


RESULT 122
Q8AW02_CYPCA
ID   Q8AW02_CYPCA   PRELIMINARY;   PRT;   231 AA.
AC   Q8AW02;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Putative Tumour necrosis factor alpha two.
GN   Name=TNF-alpha2pro;
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Head kidney;
RX   MEDLINE=22365628; PubMed=12477499; DOI=10.1016/S0145-305X(02)00064-2;
RA   Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,
RA   Wiegertjes G.F.;
RT   "Molecular and functional characterization of carp TNF: a link between
RT   TNF polymorphism with trypanotolerance?";
RL   Dev. Comp. Immunol. 27:29-41(2003).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ311801; CAC84642.2; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   231 AA;  25927 MW;  2AD8871D0B1A82F1 CRC64;

  Query Match             25.6%;  Score 201.5;  DB 2;  Length 231;
  Best Local Similarity   33.1%;  Pred. No. 8.9e-11;
  Matches   47;  Conservative   28;  Mismatches   50;  Indels   17;  Gaps    5;

Qy         26 LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTH--------VLLT 77
              | |    :  | :: |:|| | ::::|::|:| :|||| |:       |        | ::
Db         97 LDWKQNQDQAFVSGGLELVDREIIIPNDGIYFVYSQVSFH---ISCKHDMTEDQDVVHMS 153

Qy         78 HTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEIN 137
              | : | : || ::  | |||:| |   :     : ||  ||||  | | : |||  |
Db        154 HAVLRYSESYGSYKPLFSAIRSACVHASD---SEDLWYNTIYLGAAFNLRARDRLRTETT 210

Qy        138 RPDYLDFAES--GQVYFGIIAL 157
              : : |   ||  |: :||: ||
Db        211 K-ELLPRVESENGKTFFGVFAL 231


RESULT 123
Q8AWC9_CYPCA
ID   Q8AWC9_CYPCA   PRELIMINARY;   PRT;   237 AA.
AC   Q8AWC9;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   Putative tumor necrosis factor alpha one.
GN   Name=TNF-alpha;
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Head kidney;
RX   MEDLINE=22365628; PubMed=12477499; DOI=10.1016/S0145-305X(02)00064-2;
RA   Saeij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,
RA   Wiegertjes G.F.;
RT   "Molecular and functional characterization of carp TNF: a link between
RT   TNF polymorphism with trypanotolerance?";
RL   Dev. Comp. Immunol. 27:29-41(2003).
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ311800; CAC84641.2; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   237 AA;  26192 MW;  7D11D35CFC8E1664 CRC64;

  Query Match             25.6%;  Score 201.5;  DB 2;  Length 237;
  Best Local Similarity   33.3%;  Pred. No. 9.2e-11;
  Matches   48;  Conservative   32;  Mismatches   43;  Indels   21;  Gaps    7;

Qy         26 LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPST----H--VLLTHT 79
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Db        103 LDWKKNQDQAFTSGGLKLVEREIIIPTDGIYFVYSQVSFH-INCKTNMTEDHDLVHMSHT 161

Qy         80 ISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXP----WYEPIYLGGVFQLEXGDRLSAE 135

Db        162 VLRYSDSYGRYMPLFSAIRTAC-------AQASNTDDLWYNTIYLGAAFKLRAGDRLRTE 214

Qy        136 INRPDYLDFAES--GQVYFGIIAL 157

Db        215 TTE-ELLPSVETGDGKTFFGVFAL 237


RESULT 124
Q58G74_CHICK
ID   Q58G74_CHICK   PRELIMINARY;   PRT;   207 AA.
AC   Q58G74;
DT   26-APR-2005, integrated into UniProtKB/TrEMBL.
DT   26-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Vascular endothelial growth inhibitor (Fragment).
GN   Name=TNFSF15;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Limb growth discs;
RA   Tubak V., Rauch T., Duda E.G.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY954626; AAX54697.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   207 AA;  22707 MW;  CFD1A0BA238F52CC CRC64;

  Query Match             25.6%;  Score 201;  DB 2;  Length 207;
  Best Local Similarity   28.5%;  Pred. No. 8.6e-11;
  Matches   45;  Conservative   34;  Mismatches   63;  Indels   16;  Gaps    3;

Qy          9 SDXPVAHVVANPQAEGQ--------LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Db         57 AEKPRAHLTVKKQEPSSTTGSHLPILQWEDKRGLAFTKNNLSYSSNALVMPVSGDYYVYA 116

Qy         61 QVLFXGQGCPSTHV-LLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIY 119

Db        117 QVTFRGPSDTSSKTSSVTAVITKVTDSYPEPTQLLTSTKTLSE-------ERNNWFQPIY 169

Qy        120 LGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

Db        170 LGAVVSLEIGDKLMVNVSDIKLVDYTKEHKTFFGAFLL 207


RESULT 125
Q5VJK8_HUMAN
ID   Q5VJK8_HUMAN   PRELIMINARY;   PRT;   192 AA.
AC   Q5VJK8;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Vascular endothelial growth inhibitor-192A.
GN   Name=TNFSF15;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21974864; PubMed=11923219;
RA   Chew L.J., Pan H., Yu J., Tian S., Huang W.Q., Zhang J.Y., Pang S.,
RA   Li L.Y.;
RT   "A novel secreted splice variant of vascular endothelial cell growth
RT   inhibitor.";
RL   FASEB J. 16:742-744(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Li L.-Y., Pan H.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY434464; AAR98573.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   192 AA;  21857 MW;  CC7D2E73CEF5A53A CRC64;

  Query Match             25.5%;  Score 200.5;  DB 2;  Length 192;
  Best Local Similarity   27.6%;  Pred. No. 8.7e-11;
  Matches   47;  Conservative   30;  Mismatches   68;  Indels   25;  Gaps    3;

Qy          6 RTPSDXPVAHVVANPQAEGQ--------LQWLNRRANALLANGVELRDNQLVVPSEGLYL 57

Db         30 RADGDKPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYF 89

Qy         58 IYSQVLFXGQ----------GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPE 107

Db         90 IYSQVTFRGMTSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCE----- 144

Qy        108 GAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

Db        145 --VGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL 192


RESULT 126
Q3SX69_HUMAN
ID   Q3SX69_HUMAN   PRELIMINARY;   PRT;   251 AA.
AC   Q3SX69;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Tumor necrosis factor (Ligand) superfamily, member 15.
GN   Name=TNFSF15;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC104462; AAI04463.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   251 AA;  28068 MW;  08BD3E5C37A2EADD CRC64;

  Query Match             25.5%;  Score 200.5;  DB 2;  Length 251;
  Best Local Similarity   27.6%;  Pred. No. 1.2e-10;
  Matches   47;  Conservative   30;  Mismatches   68;  Indels   25;  Gaps    3;

Qy          6 RTPSDXPVAHVVANPQAEGQ--------LQWLNRRANALLANGVELRDNQLVVPSEGLYL 57
              |   |:| ||:    |   |         | | :    |   | :   :  |::|  | |
Db         89 RADGDKPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYF 148

Qy         58 IYSQVLFXGQ----------GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPE 107
              ||||| |:|           | |:    :|  |::: ||  :  ||   :| |:
Db        149 IYSQVTFRGMTSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCE----- 203

Qy        108 GAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                  : |::||||| :| |::||:|   ::    :|: :  : :||   |
Db        204 --VGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL 251


RESULT 127
Q8NFE9_HUMAN
ID   Q8NFE9_HUMAN   PRELIMINARY;   PRT;   251 AA.
AC   Q8NFE9;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 26.
DE   TNF superfamily ligand TL1A (Tumor necrosis factor (Ligand)
DE   superfamily, member 15).
GN   Name=TNFSF15; ORFNames=RP11-428F18.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21909416; PubMed=11911831; DOI=10.1016/S1074-7613(02)00283-2;
RA   Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA   Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA   Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA   Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT   "TL1A is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
RT   cell costimulator.";
RL   Immunity 16:479-492(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones, and Pooled tissue;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pooled tissue;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Babbage A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF520785; AAM77366.1; -; mRNA.
DR   EMBL; BC069435; AAH69435.1; -; mRNA.
DR   EMBL; BC074940; AAH74940.1; -; mRNA.
DR   EMBL; BC074941; AAH74941.1; -; mRNA.
DR   EMBL; AL390240; CAH73731.1; -; Genomic_DNA.
DR   EMBL; BC104463; AAI04464.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSG00000181634; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
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DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   251 AA;  28087 MW;  65ED70E367E3446D CRC64;

  Query Match             25.5%;  Score 200.5;  DB 2;  Length 251;
  Best Local Similarity   27.6%;  Pred. No. 1.2e-10;
  Matches   47;  Conservative   30;  Mismatches   68;  Indels   25;  Gaps    3;

Qy          6 RTPSDXPVAHVVANPQAEGQ--------LQWLNRRANALLANGVELRDNQLVVPSEGLYL 57
              |    |:| ||:    |   |         | | :    |   | :   :  |::|  | |
Db         89 RADGDKPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYF 148

Qy         58 IYSQVLFXGQ----------GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPE 107
              ||||| |:|           | |:    :|  |:::  ||  :  ||   :| |:
Db        149 IYSQVTFRGMTSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCE----- 203

Qy        108 GAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                  : |::||||| :| |::||:|   ::    :|: :  : :||   |
Db        204 --VGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL 251


RESULT 128
Q80YZ0_MOUSE
ID   Q80YZ0_MOUSE   PRELIMINARY;   PRT;   252 AA.
AC   Q80YZ0;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Tumor necrosis factor (Ligand) superfamily, member 15 (Vascular
DE   endothelial growth inhibitor).
GN   Name=TNFSF15; Synonyms=Tnfsf15; ORFNames=RP23-20K13.4-001;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sycamore N.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RX   PubMed=15702971;
RA   Xiao Q., Hsu C.Y., Chen H., Ma X., Xu J., Lee J.M.;
RT   "Characterization of cis-regulatory elements of the vascular
RT   endothelial growth inhibitor gene promoter.";
RL   Biochem. J. 388:913-920(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RA   Xiao Q.L., Hsu C.Y., Chen H., Ma X.C., Xu J., Lee J.-M.;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/He mice; TISSUE=Osteoblast;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/He mice; TISSUE=Osteoblast;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AL691468; CAD83021.1; -; Genomic_DNA.
DR   EMBL; AY764130; AAV33431.1; -; mRNA.
DR   EMBL; BC096494; AAH96494.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSMUSG00000050395; Mus musculus.
DR   MGI; MGI:2180140; Tnfsf15.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   252 AA;  27725 MW;  A63ABDCC9E969E0F CRC64;

  Query Match             25.4%;  Score 199.5;  DB 2;  Length 252;
  Best Local Similarity   28.0%;  Pred. No. 1.6e-10;
  Matches   47;  Conservative   31;  Mismatches   65;  Indels   25;  Gaps    4;

Qy          8 PSDXPVAHVVANPQAE--------GQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              |  :| ||:    |             | | :    |   ||::  :  ||:|  | | ||
Db         92 PRGKPRAHLTIKKQTPAPHLKNQLSALHWEHDLGMAFTKNGMKYINKSLVIPESGDYFIY 151

Qy         60 SQVLFXG--QGC--------PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGA 109
              ||: |:|    |         |:    :|  |:::| ||  :  ||:  :| |:
Db        152 SQITFRGTTSVCGDISRGRRPNKPDSITMVITKVADSYPEPARLLTGSKSVCE------- 204

Qy        110 EAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               :: |:: :|||  | ||:||||   ::    :|: :  : :||   |
Db        205 ISNNWFQSLYLGATFSLEEGDRLMVNVSDISLVDYTKEDKTFFGAFLL 252


RESULT 129
Q8K3Y8_MOUSE
ID   Q8K3Y8_MOUSE   PRELIMINARY;   PRT;   252 AA.
AC   Q8K3Y8;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   TNF superfamily ligand TL1A.
GN   Name=Tnfsf15;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   MEDLINE=21909416; PubMed=11911831; DOI=10.1016/S1074-7613(02)00283-2;
RA   Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA   Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA   Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA   Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT   "TL1A is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
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RT   cell costimulator.";
RL   Immunity 16:479-492(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF520786; AAM77367.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSMUSG00000050395; Mus musculus.
DR   MGI; MGI:2180140; Tnfsf15.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   252 AA;  27723 MW;  BB901C9350119E0F CRC64;

  Query Match             25.4%;  Score 199.5;  DB 2;  Length 252;
  Best Local Similarity   28.0%;  Pred. No. 1.6e-10;
  Matches   47;  Conservative   32;  Mismatches   64;  Indels   25;  Gaps    4;

Qy          8 PSDXPVAHVVANPQAE--------GQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              |  :| ||:     |             | | :    |   ||::  :  ||:|  | | ||
Db         92 PRGKPRAHLTIKKQTPAPHLKNQLSALHWEHDLGMAFTKNGMKYINKSLVIPESGDYFIY 151

Qy         60 SQVLFXG--QGC--------PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGA 109
              ||: |:|    |         |:    :|  |:::| ||  :  ||:  :| |:
Db        152 SQITFRGTTSVCGDISRGRRPNKPDSITVVITKVADSYPEPARLLTGSKSVCE------- 204

Qy        110 EAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                :: |:: :||| :| ||:||||   ::    :|: :  : :||   |
Db        205 ISNNWFQSLYLGAMFSLEEGDRLMVNVSDISLVDYTKEDKTFFGAFLL 252


RESULT 130
Q5I6M8_SALSA
ID   Q5I6M8_SALSA   PRELIMINARY;   PRT;   160 AA.
AC   Q5I6M8;
DT   15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT   15-FEB-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ingerslev H.-C., Cunningham C., Wergeland H.;
RT   "Cloning and expression of TNF-alpha, IL-1 and COX-2 in an anadromous
RT   and landlocked strain of Atlantic salmon (Salmo salar L.) in the
RT   smolting period.";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY848945; AAW31869.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
FT   NON_TER     160     160
SQ   SEQUENCE   160 AA;  17832 MW;  1493A90EAE70923E CRC64;

  Query Match             25.2%;  Score 198;  DB 2;  Length 160;
  Best Local Similarity   34.0%;  Pred. No. 1.2e-10;
  Matches   49;  Conservative   25;  Mismatches   62;  Indels    8;  Gaps    5;

Qy         19 NPQ-AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPS---THV 74
              ||      :||       |    | :|: ||:::|  ||: :|||  |: : | |
Db         19 NPNLTANTVQWRKDDGQAFSQGGFKLQGNQILIPHTGLFFVYSQASFRVK-CNSPGERTT 77

Qy         75 LLTHTISRIAVSYQTXVNLLSAIXSPCQRE--TPEGAEAXPWYEPIYLGGVFQLEXGDRL 132
               |:| | | : |   : |||| ::| ||:     |    : ||  :||  || | :||:|
Db         78 PLSHVIWRYSDSIGDNANLLSGVRSVCQQNYGNSESNIGEGWYNAVYLSAVFHLNEGDKL 137

Qy        133 SAEINRPDYLDFAESGQVYFGIIA 156
             •   | ||   ::  | |: :||: |
Db        138 WTETNRLTEVE-PEQGKNFFGVFA 160


RESULT 131
Q8JG37_ICTPU
ID   Q8JG37_ICTPU   PRELIMINARY;   PRT;   230 AA.
AC   Q8JG37;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 2.
DT   07-FEB-2006, entry version 14.
DE   Tumor necrosis factor.
GN   Name=TNF;
OS   Ictalurus punctatus (Channel catfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC   Ictaluridae; Ictalurus.
OX   NCBI_TaxID=7998;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Zou J., Chinchar G., Long S., Miller N., Secombes C.J.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ417565; CAD10389.2; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   230 AA;  25598 MW;  3A40D391F75DB019 CRC64;

  Query Match             24.9%;  Score 195.5;  DB 2;  Length 230;
  Best Local Similarity   32.4%;  Pred. No. 3.3e-10;
  Matches   48;  Conservative   33;  Mismatches   54;  Indels   13;  Gaps    6;

Qy         19 NPQAEG-QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF------XGQGCPS 71
              |||      :|| :  |:   ::|::| ||:: :  :||| :|||  :       :|
Db         87 NPQVSSVSMQWFD-NADQSFSSGLKLEDNEIKILRDGLYFVYSQASYRLLCKAEGDETEG 145

Qy         72 THVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDR 131
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Db        146 EVMHMSHKVSRWSDSYSSWKPLLSATRSACKKTTEE--YQKYWYGAVYLGAAFNLKAGDR 203

Qy        132 LSAEINRPDYLDFAES--GQVYFGIIAL 157
Db        204 LRTVMDE-KLLPKVESAGGKTFFGTFSL 230


RESULT 132
Q7ZZX5_PAGMA
ID   Q7ZZX5_PAGMA   PRELIMINARY;   PRT;   110 AA.
AC   Q7ZZX5;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   TNFa (Fragment).
OS   Pagrus major (Red sea bream) (Chrysophrys major).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sparidae; Pagrus.
OX   NCBI_TaxID=143350;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Cai Z., Song L., Xiang J., Qiu L., Gao C.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AY243108; AAP23260.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   110 AA;  12190 MW;  E5CE3C7ACA170381 CRC64;

  Query Match             24.8%;  Score 195;  DB 2;  Length 110;
  Best Local Similarity   38.7%;  Pred. No. 1.4e-10;
  Matches   43;  Conservative   21;  Mismatches   37;  Indels   10;  Gaps    3;

Qy         56 YLIYSQVLF-------XGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEG 108
Db          1 YFVYSQASFRVSCSDGEEEGAGGHHTPLSHRISRSSESMGSDVSLMSAVRSACQNTAQDD 60

Qy        109 --AEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db         61 SYSDGRGWYNTIYLGAVFQLNRGDRLWTETNQLSELE-TEEGKTFFGVFAL 110


RESULT 133
Q9XT69_CANFA
ID   Q9XT69_CANFA   PRELIMINARY;   PRT;   41 AA.
AC   Q9XT69;
DT   01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1999, sequence version 1.
DT   07-FEB-2006, entry version 22.
DE   TNFA (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99265967; PubMed=10331940; DOI=10.1006/geno.1999.5772;
RA   Li R., Mignot E., Faraco J., Kadotani H., Cantanese J., Zhao B.,
RA   Lin X., Hinton L., Ostrander E.A., Patterson D.F., de Jong P.J.;
RT   "Construction and characterization of an eightfold redundant dog
RT   genomic bacterial artificial chromosome library.";
RL   Genomics 58:9-17(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Kodatani H., Mignot E.;
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF103743; AAD40571.1; -; Genomic_DNA.
DR   HSSP; P01375; 1TNF.
DR   Ensembl; ENSCAFG00000000517; Canis familiaris.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER      41     41
SQ   SEQUENCE   41 AA;  4437 MW;  64C83319CC6AB473 CRC64;

  Query Match             24.6%;  Score 193;  DB 2;  Length 41;
  Best Local Similarity   90.2%;  Pred. No. 5.8e-11;
  Matches   37;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQL 48
Db          1 PSDKPVAHVVANPEAEGQLQWLTRRANALLANGVELTDNQL 41


RESULT 134
TNF15_HUMAN
ID   TNF15_HUMAN    STANDARD;      PRT;   174 AA.
AC   O95150;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1999, sequence version 1.
DT   07-FEB-2006, entry version 35.
DE   Tumor necrosis factor ligand superfamily member 15 (Vascular
DE   endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
GN   Name=TNFSF15; Synonyms=TL1, VEGI;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Umbilical vein;
RX   MEDLINE=99091541; PubMed=9872942;
RA   Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,
RA   Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,
RA   Li L.-Y., Gentz R., Yu G.-L.;
RT   "VEGI, a novel cytokine of the tumor necrosis factor family, is an
RT   angiogenesis inhibitor that suppresses the growth of colon carcinomas
RT   in vivo.";
RL   FASEB J. 13:181-189(1999).
CC   -!- FUNCTION: Inhibits vascular endothelial growth and angiogenesis
CC       (in vitro).
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Probable).
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CC   -!- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
CC       Detected in placenta, lung, kidney, skeletal muscle, pancreas,
CC       spleen, prostate, small intestine and colon.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF039390; AAD08783.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   HGNC; HGNC:11931; TNFSF15.
DR   MIM; 604052; gene.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0000074; P:regulation of progression through cell cycle; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    174       Tumor necrosis factor ligand superfamily
FT                                member 15.
FT                                /FTId=PRO_0000185505.
FT   TOPO_DOM      1     12       Cytoplasmic (Potential).
FT   TRANSMEM     13     25       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     26    174       Extracellular (Potential).
FT   CARBOHYD     56     56       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    152    152       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     85    125       Potential.
SQ   SEQUENCE   174 AA;  20131 MW;  CCB83BA7EE673B98 CRC64;

  Query Match             23.5%;  Score 185;  DB 1;  Length 174;
  Best Local Similarity   26.9%;  Pred. No. 2.4e-09;
  Matches   43;  Conservative   30;  Mismatches   67;  Indels   20;  Gaps    3;

Qy         11 XPVAHVVANPQAEGQ---LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              :||         : |   | | :    |   | :   :  |::|  | | |||||  |:|
Db         22 FPVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGM 81

Qy         68 ----------GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEP 117
                        | |:    :|  |:::  ||  :  ||   :| |:         : |::|
Db         82 TSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCE-------VGSNWFQP 134

Qy        118 IYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||| :| |::||:|   ::    :|: :  : :||   |
Db        135 IYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL 174


RESULT 135
Q5VWH1_HUMAN
ID   Q5VWH1_HUMAN   PRELIMINARY;   PRT;   174 AA.
AC   Q5VWH1;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Tumor necrosis factor (Ligand) superfamily, member 15.
GN   Name=TNFSF15; ORFNames=RP11-428F18.1-002;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Babbage A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AL390240; CAH73730.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   174 AA;  20112 MW;  60C9ED707832A90B CRC64;

  Query Match             23.5%;  Score 185;  DB 2;  Length 174;
  Best Local Similarity   26.9%;  Pred. No. 2.4e-09;
  Matches   43;  Conservative   30;  Mismatches   67;  Indels   20;  Gaps    3;

Qy         11 XPVAHVVANPQAEGQ---LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              :||         : |   | | :    |   | :   :  |::|  | | |||||  |:|
Db         22 FPVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGM 81

Qy         68 ----------GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEP 117
                        | |:    :|  |:::  ||  :  ||   :| |:         : |::|
Db         82 TSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCE-------VGSNWFQP 134

Qy        118 IYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||| :| |::||:|   ::    :|: :  : :||   |
Db        135 IYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL 174


RESULT 136
Q4W898_BRARE
ID   Q4W898_BRARE   PRELIMINARY;   PRT;   242 AA.
AC   Q4W898;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Tumor necrosis factor alpha.
GN   Name=tnf; Synonyms=TNF alpha;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15759114; DOI=10.1007/s00251-005-0768-4;
RA   Savan R., Kono R., Igawa D., Sakai M.;
RT   "A novel tumor necrosis factor (TNF) gene present in tandem with
RT   theTNF-alpha gene on the same chromosome in teleosts.";
RL   Immunogenetics 57:140-150(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Ram S., Sakai M.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AB183467; BAD98730.1; -; mRNA.
DR   ZFIN; ZDB-GENE-050601-2; tnf.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
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DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   242 AA;  26765 MW;  AAF7E7F112A2BEBD CRC64;

  Query Match             23.1%;  Score 181.5;  DB 2;  Length 242;
  Best Local Similarity   28.7%;  Pred. No. 8e-09;
  Matches   45;  Conservative   33;  Mismatches   60;  Indels   19;  Gaps    5;

Qy          9 SDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF---- 64
              |  :   |:  :|  :  |:|:     |    |: | :|::::| :||| :|||| :
Db         97 STKAAIHLHGDPSGQ-SLKWVGGVDQAFQQGGLRLENNEIIIPKDGLYFVYSQVSYETLC 155

Qy         65 ----XGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
                :| |       |:|||:|   : : :: | :: :| ||       : :  |  |||
Db        156 VEDVEGDG----QKYLSHTINRYTDAVREKMPLQNSANSVCQ-----SLDGKTSYSTIYL 206

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              | || | : ||||    |   ::     : :||: ||
Db        207 GAVFDLFGDDRLSTHTTRVGDIE-NNYAKTFFGVFAL 242


RESULT 137
Q5CAQ0_CHICK
ID   Q5CAQ0_CHICK   PRELIMINARY;   PRT;   253 AA.
AC   Q5CAQ0;
DT   12-APR-2005, integrated into UniProtKB/TrEMBL.
DT   12-APR-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   FAS ligand.
GN   Name=TNFSF6;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Reddy S.K., Snell D.C., Young J.R.;
RT   "Structure and expression of chicken TNFSF6 (FASL) gene.";
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ890143; CAI64582.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006052; TNF_family.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   253 AA;  28831 MW;  ED6FB6A82C8627C2 CRC64;

  Query Match             22.8%;  Score 179.5;  DB 2;  Length 253;
  Best Local Similarity   32.2%;  Pred. No. 1.3e-08;
  Matches   47;  Conservative   30;  Mismatches   56;  Indels   13;  Gaps    6;

Qy         14 AHVVANP-QAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPST 72
              ||:  || |    |:|     :|   :|:: ||  ||:   ||| :|| |||:|: | :
Db        119 AHLTGNPTQRNLPLEWEPVSGHA-FTSGIQYRDQGLVINETGLYFVYSNVLFRGRHCDNE 177

Qy         73 HVLLTHTI-SRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDR 131
                :||| :  |   |  ::| :    :: | :|       : |    ||| :|:| : |

Db        178 --VLTHVVYKRNPASPGSHVLMEDKRINYCTKE-------KMWARKSYLGALFKLRERDS 228

Qy        132 LSAEINRPDYLDFAESGQVYFGIIAL 157
                |   ::| | ::| || : :||:  |
Db        229 LYVNVSRIDLVNFEES-KTFFGLFKL 253


RESULT 138
TNF14_HUMAN
ID   TNF14_HUMAN    STANDARD;      PRT;   240 AA.
AC   O43557; O75476; Q8WVF8; Q96LD2;
DT   21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1998, sequence version 1.
DT   07-FEB-2006, entry version 54.
DE   Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
DE   mediator-ligand) (HVEM-L) (CD258 antigen) [Contains: Tumor necrosis
DE   factor ligand superfamily member 14, membrane form; Tumor necrosis
DE   factor ligand superfamily member 14, soluble form].
GN   Name=TNFSF14; Synonyms=HVEML, LIGHT; ORFNames=UNQ391/PRO726;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX   MEDLINE=98122340; PubMed=9462508; DOI=10.1016/S1074-7613(00)80455-0;
RA   Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
RA   Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA   Ware C.F.;
RT   "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT   ligands for herpesvirus entry mediator.";
RL   Immunity 8:21-30(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND CHARACTERIZATION.
RC   TISSUE=Liver;
RX   MEDLINE=98438532; PubMed=9765287; DOI=10.1074/jbc.273.42.27548;
RA   Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA   Tan K.B., Dede K., Spampanato J.,,Silverman C., Hensley P.,
RA   DiPrinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA   Truneh A., Young P.R.;
RT   "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RT   HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 cell
RT   growth.";
RL   J. Biol. Chem. 273:27548-27556(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND PROCESSING.
RX   MEDLINE=21528948; PubMed=11673523;
RA   Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
RT   "Genomic characterization of LIGHT reveals linkage to an immune
RT   response locus on chromosome 19p13.3 and distinct isoforms generated
RT   by alternate splicing or proteolysis.";
RL   J. Immunol. 167:5122-5128(2001).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
CC       decoy receptor TNFRSF6B modulates its effects. Activates NFKB,
CC       stimulates the proliferation of T cells, and inhibits growth of
CC       the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
CC       virus.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- INTERACTION:
CC       O95407:TNFRSF6B; NbExp=1; IntAct=EBI-524131, EBI-524171;
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC       (isoform 1); Cytoplasmic (isoform 2).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=O43557-1; Sequence=Displayed;
CC       Name=2; Synonyms=LIGHT delta-TM;
CC         IsoId=O43557-2; Sequence=VSP_006452;
CC   -!- TISSUE SPECIFICITY: Predominantly expressed in the spleen but also
CC       found in the brain. Weakly expressed in peripheral lymphoid
CC       tissues and in heart, placenta, liver, lung, appendix, and kidney,
CC       and no expression seen in fetal tissues, endocrine glands, or
CC       nonhematopoietic tumor lines.
CC   -!- INDUCTION: Up-regulated after T-cell activation.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC       by proteolytic processing.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   -!- CAUTION: Ref.5 sequence differs from that shown due to a
CC       frameshift in position 178.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF036581; AAC39563.1; -; mRNA.
DR   EMBL; AF064090; AAC25169.1; -; mRNA.
DR   EMBL; AY028261; AAK26160.1; -; mRNA.
DR   EMBL; AY358812; AAQ89171.1; -; mRNA.
DR   EMBL; BC018058; AAH18058.1; ALT_FRAME; mRNA.
DR   HSSP; P01375; 4TSV.
DR   IntAct; O43557; -.
DR   Ensembl; ENSG00000125735; Homo sapiens.
DR   H-InvDB; HIX0019691; -.
DR   HGNC; HGNC:11930; TNFSF14.
DR   MIM; 604520; gene.
DR   GO; GO:0043027; F:caspase inhibitor activity; IDA.
DR   GO; GO:0005102; F:receptor binding; IPI.
DR   GO; GO:0006917; P:induction of apoptosis; TAS.
DR   GO; GO:0001719; P:inhibition of caspase activation; IDA.
DR   GO; GO:0008588; P:release of cytoplasmic sequestered NF-kappaB; IDA.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   GO; GO:0043029; P:T cell homeostasis; NAS.
DR   GO; GO:0042098; P:T cell proliferation; NAS.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Alternative splicing; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    240       Tumor necrosis factor ligand superfamily
FT                                member 14, membrane form.
FT                                /FTId=PRO_0000034532.
FT   CHAIN       ?83    240       Tumor necrosis factor ligand superfamily
FT                                member 14, soluble form.
FT                                /FTId=PRO_0000034533.
FT   TOPO_DOM      1     37       Cytoplasmic (Potential).
FT   TRANSMEM     38     58       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     59    240       Extracellular (Potential).
FT   SITE         82     83       Cleavage (Potential).
FT   CARBOHYD    102    102       N-linked (GlcNAc. . .).
FT   DISULFID    154    187       Potential.
FT   VARSPLIC     38     73       Missing (in isoform 2).
FT                                /FTId=VSP_006452.
FT   CONFLICT    120    120       L -> V (in Ref. 5).
FT   CONFLICT    214    214       E -> K (in Ref. 2).
SQ   SEQUENCE   240 AA;  26351 MW;  49D0BF67E1390B39 CRC64;

  Query Match             22.6%;  Score 177.5;  DB 1;  Length 240;
  Best Local Similarity   31.4%;  Pred. No. 1.9e-08;
  Matches   49;  Conservative   28;  Mismatches   64;  Indels   15;  Gaps    6;

Qy          6 RTPSDXPVAHVV-ANPQ---AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
              |:   :| ||:  ||      : | | |  :   | |  |:   |  |||   | | |||:
Db         88 RSHEVNPAAHLTGANSSLTGSGGPLLWETQLGLAFL-RGLSYHDGALVVTKAGYYYIYSK 146

Qy         62 VLFXGQGCP----STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEP 117
              |  :| |||    ||   :|| : :    |  :: || : :||| | |   : :: |::
Db        147 VQLGGVGCPLGLAST---ITHGLYKRTPRYPEELELLVSQQSPCGRAT---SSSRVWWDS 200

Qy        118 IYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
                :|||| ||:|: :   :     :   : : |||
Db        201 SFLGGVVHLEAGEEVVVRVLDERLVRLRDGTRSYFG 236


RESULT 139
Q6FHA1_HUMAN
ID   Q6FHA1_HUMAN   PRELIMINARY;   PRT;   240 AA.
AC   Q6FHA1;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   TNFSF14 protein.
GN   Name=TNFSF14;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CR541854; CAG46652.1; -; mRNA.
DR   EMBL; CR541871; CAG46669.1; -; mRNA.
DR   Ensembl; ENSG00000125735; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
```

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DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   240 AA;  26351 MW;  49D0BF67E1390B39 CRC64;

  Query Match             22.6%;  Score 177.5;  DB 2;  Length 240;
  Best Local Similarity   31.4%;  Pred. No. 1.9e-08;
  Matches   49;  Conservative   28;  Mismatches   64;  Indels   15;  Gaps    6;

Qy          6 RTPSDXPVAHVV-ANPQ---AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
              |:   :| ||:  ||      : | | |  :   | |  |:   |  |||   | | |||:
Db         88 RSHEVNPAAHLTGANSSLTGSGGPLLWETQLGLAFL-RGLSYHDGALVVTKAGYYYIYSK 146

Qy         62 VLFXGQGCP----STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEP 117
              |  :| |||    ||   :|| : :    |  :: || : :||| | |   : :: |::
Db        147 VQLGGVGCPLGLAST---ITHGLYKRTPRYPEELELLVSQQSPCGRAT---SSSRVWWDS 200

Qy        118 IYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
              :||||  ||:|: :   :     :  :  : |||
Db        201 SFLGGVVHLEAGEEVVVRVLDERLVRLRDGTRSYFG 236


RESULT 140
TNFC_HUMAN
ID   TNFC_HUMAN     STANDARD;      PRT;   244 AA.
AC   Q06643; P78370; Q99761;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 1.
DT   07-FEB-2006, entry version 55.
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   Name=LTB; Synonyms=TNFC, TNFSF3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1), AND PARTIAL PROTEIN SEQUENCE.
RC   TISSUE=T-cell;
RX   MEDLINE=93208881; PubMed=7916655; DOI=10.1016/0092-8674(93)90574-A;
RA   Browning J.L., Ngam-Ek A., Lawton P., Demarinis J., Tizard R.,
RA   Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
RT   "Lymphotoxin beta, a novel member of the TNF family that forms a
RT   heteromeric complex with lymphotoxin on the cell surface.";
RL   Cell 72:847-856(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RX   MEDLINE=97445965; PubMed=9299492; DOI=10.1006/bbrc.1997.7277;
RA   Warzocha K., Renard N., Charlot C., Bienvenu J., Coiffier B.,
RA   Salles G.;
RT   "Identification of two lymphotoxin beta isoforms expressed in human
RT   lymphoid cell lines and non-Hodgkin's lymphomas.";
RL   Biochem. Biophys. Res. Commun. 238:273-276(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX   MEDLINE=99218514; PubMed=10202016;
RA   Neville M.J., Campbell R.D.;
RT   "A new member of the Ig superfamily and a V-ATPase G subunit are among
RT   the predicted products of novel genes close to the TNF locus in the
RT   human MHC.";
RL   J. Immunol. 162:4745-4754(1999).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=14656967; DOI=10.1101/gr.1736803;
RA   Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA   Campbell R.D., Hood L.;
RT   "Analysis of the gene-dense major histocompatibility complex class III
RT   region and its comparison to mouse.";
RL   Genome Res. 13:2621-2636(2003).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Shiina S., Tamiya G., Oka A., Inoko H.;
RT   "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLU-70 AND PRO-111.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ARG-84 AND PHE-87.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface. Isoform 2 is probably non-functional.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) one LTB and two LTA subunits.
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q06643-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q06643-2; Sequence=VSP_006441, VSP_006442;
CC   -!- TISSUE SPECIFICITY: Spleen and thymus.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; L11016; AAA99888.1; -; Genomic_DNA.
DR   EMBL; U89922; AAC51769.1; -; mRNA.
DR   EMBL; U79029; AAB37342.1; -; mRNA.
DR   EMBL; L11015; AAA36191.1; -; mRNA.
DR   EMBL; Y14768; CAA75069.1; -; Genomic_DNA.
DR   EMBL; AF129756; AAD18089.1; -; Genomic_DNA.
DR   EMBL; BA000025; BAB63395.1; -; Genomic_DNA.
DR   EMBL; AY070219; AAL49954.1; -; Genomic_DNA.
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DR   EMBL; AY070219; AAL49955.1; -; Genomic_DNA.
DR   EMBL; AY216497; AAO21134.1; -; Genomic_DNA.
DR   EMBL; BC069330; AAH69330.1; -; mRNA.
DR   PIR; A46066; A46066.
DR   PIR; JC5645; JC5645.
DR   HSSP; P01374; 1TNR.
DR   Ensembl; ENSG00000096158; Homo sapiens.
DR   HGNC; HGNC:6711; LTB.
DR   MIM; 600978; gene.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Alternative splicing; Cytokine; Direct protein sequencing;
KW   Glycoprotein; Membrane; Polymorphism; Signal-anchor; Transmembrane.
FT   CHAIN         1    244       Lymphotoxin-beta.
FT                                /FTId=PRO_0000185486.
FT   TOPO_DOM      1     18       Cytoplasmic (Potential).
FT   TRANSMEM     19     48       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     49    244       Extracellular (Potential).
FT   CARBOHYD    222    222       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     53     77       GLVTETADPGAQAQQGLGFQKLPEE -> GLGFRSCQRRSQ
FT                                KQISAPGSQLPTS (in isoform 2).
FT                                /FTId=VSP_006441.
FT   VARSPLIC     78    244       Missing (in isoform 2).
FT                                /FTId=VSP_006442.
FT   VARIANT      70     70       G -> E (in dbSNP:3093554).
FT                                /FTId=VAR_013025.
FT   VARIANT      84     84       S -> R (in dbSNP:4647186).
FT                                /FTId=VAR_016331.
FT   VARIANT      87     87       L -> F (in dbSNP:4647187).
FT                                /FTId=VAR_016332.
FT   VARIANT     111    111       A -> P (in dbSNP:3093555).
FT                                /FTId=VAR_013026.
FT   CONFLICT     60     69       DPGAQAQQGL -> GLSAPGSGRT (in Ref. 2;
FT                                AAB37342).
SQ   SEQUENCE   244 AA;  25390 MW;  F41569459830ED4C CRC64;

  Query Match             22.5%;  Score 177;  DB 1;  Length 244;
  Best Local Similarity   26.2%;  Pred. No. 2.2e-08;
  Matches   42;  Conservative   34;  Mismatches   64;  Indels   20;  Gaps    5;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ-LVVPSEGLYLIYSQVLFXGQGC 69
              :| ||::  |     | |   :  | | :| :  | : | :| :||| :|  | ::|:
Db         87 LPAAHLIGAPLKGQGLGWETTKEQAFLTSGTQFSDAEGLALPQDGLYYLYCLVGYRGRAP 146

Qy         70 P------STHVLLTHTISRIAVSY--------QTXVNLLSAIXSPCQRETPEGAEAXPWY 115
              |          | |  :: |   :|          :   :: :: | :|:       : ||
Db        147 PGGGDPQGRSVTLRSSLYRAGGAYGPGTPELLLEGAETVTPVLDPARRQ----GYGPLWY 202

Qy        116 EPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
                :  ||: || :|:|:   |: || :|||  |: :|| :
Db        203 TSVGFGGLVQLRRGERVYVNISHPDMVDFAR-GKTFFGAV 241


RESULT 141
Q5STB2_HUMAN
ID   Q5STB2_HUMAN    PRELIMINARY;    PRT;   244 AA.
AC   Q5STB2;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-MAR-2006, entry version 10.
DE   Lymphotoxin beta (TNF superfamily, member 3).
GN   Name=LTB; ORFNames=DAQB-87N14.4-001, DASS-280D8.4-001,
GN   XXbac-BCX270M2.8-001, XXbac-BPG296P20.7-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
RT   "Genome diversity in HLA: A new strategy for detection of genetic
RT   polymorphisms in expressed genes within the HLA class III and class I
RT   regions.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood leukocyte;
RA   Shiina T., Ota M., Takasu M., Katsuyama Y., Hashimoto N., Tokunaga K.,
RA   Inoko H.;
RT   "Genome diversity in HLA: A new strategy for detection of genetic
RT   polymorphisms in expressed genes within the HLA class III and class I
RT   regions.";
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AL662847; CAI17679.1; -; Genomic_DNA.
DR   EMBL; AB088106; BAC54938.1; -; Genomic_DNA.
DR   EMBL; AL662801; CAI18293.1; -; Genomic_DNA.
DR   EMBL; AL929587; CAI18650.1; -; Genomic_DNA.
DR   EMBL; BX248519; CAI41941.1; -; Genomic_DNA.
DR   EMBL; AB202114; BAE78640.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000096158; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   244 AA;  25390 MW;  F41569459830ED4C CRC64;

  Query Match             22.5%;  Score 177;  DB 2;  Length 244;
  Best Local Similarity   26.2%;  Pred. No. 2.2e-08;
  Matches   42;  Conservative   34;  Mismatches   64;  Indels   20;  Gaps    5;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ-LVVPSEGLYLIYSQVLFXGQGC 69
              :| ||::  |     | |   :  | | :| :  | : | :| :||| :|  | ::|:
Db         87 LPAAHLIGAPLKGQGLGWETTKEQAFLTSGTQFSDAEGLALPQDGLYYLYCLVGYRGRAP 146

Qy         70 P------STHVLLTHTISRIAVSY--------QTXVNLLSAIXSPCQRETPEGAEAXPWY 115
              |          | |  :: |   :|          :   :: :: | :|:       : ||
Db        147 PGGGDPQGRSVTLRSSLYRAGGAYGPGTPELLLEGAETVTPVLDPARRQ----GYGPLWY 202

Qy        116 EPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
                :  ||: || :|:|:   |: || :|||  |: :|| :
Db        203 TSVGFGGLVQLRRGERVYVNISHPDMVDFAR-GKTFFGAV 241


RESULT 142
TNFL6_RAT
ID   TNFL6_RAT      STANDARD;      PRT;   278 AA.
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AC   P36940;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-1994, sequence version 1.
DT   07-FEB-2006, entry version 48.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (CD95L protein) [Contains: Tumor necrosis
DE   factor ligand superfamily member 6, membrane form; Tumor necrosis
DE   factor ligand superfamily member 6, soluble form].
GN   Name=Faslg; Synonyms=AptlLg1, Fasl, Tnfsf6;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=94084792; PubMed=7505205; DOI=10.1016/0092-8674(93)90326-L;
RA   Suda T., Takahashi T., Golstein P., Nagata S.;
RT   "Molecular cloning and expression of the Fas ligand, a novel member of
RT   the tumor necrosis factor family.";
RL   Cell 75:1169-1178(1993).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- TISSUE SPECIFICITY: Expressed in activated splenocytes and
CC       thymocytes. Moderate or weak expression found in small intestines,
CC       kidney and lung.
CC   -!- INDUCTION: By PMA/ionomycin and concavalin/interleukin-2.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U03470; AAC52129.1; -; mRNA.
DR   PIR; A49266; A49266.
DR   HSSP; P50591; 1DG6.
DR   Ensembl; ENSRNOG00000002978; Rattus norvegicus.
DR   RGD; 3880; Tnfsf6.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    278       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034512.
FT   CHAIN       127    278       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000034513.
FT   TOPO_DOM      1     77       Cytoplasmic (Potential).
FT   TRANSMEM     78     99       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    100    278       Extracellular (Potential).
FT   COMPBIAS      4     69       Pro-rich.
FT   COMPBIAS     45     58       Poly-Pro.
FT   SITE        126    127       Cleavage (By similarity).
FT   CARBOHYD    116    116       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    247    247       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    257    257       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    199    230       Potential.
SQ   SEQUENCE   278 AA;  31140 MW;  2898E18A862CEAC6 CRC64;

  Query Match             22.5%;  Score 176.5;  DB 1;  Length 278;
  Best Local Similarity   29.9%;  Pred. No. 2.9e-08;
  Matches   46;  Conservative   31;  Mismatches   66;  Indels   11;  Gaps    5;

Qy          5 SRTPSDXPVAHVVANPQAEG-QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              | |   : |||:  ||::    |:| :    ||: :||: :   ||:   ||| :||:|
Db        135 SETKKPRSVAHLTGNPRSRSIPLEWEDTYGTALI-SGVKYKKGGLVINEAGLYFVYSKVY 193

Qy         64 FXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              |:|| | |    |:| :      |  :: |:       :::       : |    ||| |
Db        194 FRGQSCNSQP--LSHKVYMRNFKYPGDLVLME------EKKLNYCTTGQIWAHSSYLGAV 245

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              | | : | |   |::   ::| || : :||:  |
Db        246 FNLTVADHLYVNISQLSLINFEES-KTFFGLYKL 278


RESULT 143
TNFL6_MACFA
ID   TNFL6_MACFA    STANDARD;      PRT;   280 AA.
AC   P63308; Q9BDM5; Q9MYL6;
DT   11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (CD95L protein) [Contains: Tumor necrosis
DE   factor ligand superfamily member 6, membrane form; Tumor necrosis
DE   factor ligand superfamily member 6, soluble form].
GN   Name=FASLG; Synonyms=CD95L, FASL, TNFSF6;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   PubMed=12957408; DOI=10.1016/S0022-1759(03)00187-X;
RA   Kirii Y., Inoue T., Yoshino K., Kayagaki N., Yagita H., Okumura K.,
RA   Shibata H., Yoshikawa Y., Terao K.;
RT   "Molecular cloning, functional characterization, and enzyme-linked
RT   immunosorbent assay of cynomolgus monkey Fas ligand.";
RL   J. Immunol. Methods 278:201-209(2003).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB035138; BAA90294.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
```

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DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    280       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034502.
FT   CHAIN       129    280       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000034503.
FT   TOPO_DOM      1     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    101       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    102    280       Extracellular (Potential).
FT   COMPBIAS      4     69       Pro-rich.
FT   COMPBIAS     45     64       Poly-Pro.
FT   SITE        128    129       Cleavage (By similarity).
FT   CARBOHYD    183    183       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    249    249       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    259    259       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    201    232       Potential.
SQ   SEQUENCE   280 AA;  31368 MW;  F0B284D61A132EB4 CRC64;

  Query Match             22.4%;  Score 176;  DB 1;  Length 280;
  Best Local Similarity   30.8%;  Pred. No. 3.3e-08;
  Matches   49;  Conservative   28;  Mismatches   62;  Indels   20;  Gaps    7;

Qy          8 PSDXP-------VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              || :|       |||:   | :    |:| :     || :||: :   ||:   ||| :|
Db        133 PSPPPEKKEQRKVAHLTGKPNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVY 191

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
              |:| |:|| |  |:: |:| :      | | :| :   ::| |          : |
Db        192 SKVYFRGQSC--TNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-------TTGQMWAHSS 242

Qy        119 YLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||| || | : | |   ::    ::| || | :||:  |
Db        243 YLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 280


RESULT 144
TNFL6_MACMU
ID   TNFL6_MACMU    STANDARD;      PRT;   280 AA.
AC   P63307; Q9BDM5; Q9MYL6;
DT   11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (CD95L protein) [Contains: Tumor necrosis
DE   factor ligand superfamily member 6, membrane form; Tumor necrosis
DE   factor ligand superfamily member 6, soluble form].
GN   Name=FASLG; Synonyms=CD95L, FASL, TNFSF6;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lymphocyte;
RX   MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA   Villinger F.J., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   PubMed=12957408; DOI=10.1016/S0022-1759(03)00187-X;
RA   Kirii Y., Inoue T., Yoshino K., Kayagaki N., Yagita H., Okumura K.,
RA   Shibata H., Yoshikawa Y., Terao K.;
RT   "Molecular cloning, functional characterization, and enzyme-linked
RT   immunosorbent assay of cynomolgus monkey Fas ligand.";
RL   J. Immunol. Methods 278:201-209(2003).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF344856; AAK37539.1; -; mRNA.
DR   EMBL; AB035139; BAA90295.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    280       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034504.
FT   CHAIN       129    280       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000034505.
FT   TOPO_DOM      1     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    101       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    102    280       Extracellular (Potential).
FT   COMPBIAS      4     69       Pro-rich.
FT   COMPBIAS     45     64       Poly-Pro.
FT   SITE        128    129       Cleavage (By similarity).
FT   CARBOHYD    183    183       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    249    249       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    259    259       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    201    232       Potential.
FT   CONFLICT     60     60       S -> P (in Ref. 1).
SQ   SEQUENCE   280 AA;  31368 MW;  F0B284D61A132EB4 CRC64;

  Query Match             22.4%;  Score 176;  DB 1;  Length 280;
  Best Local Similarity   30.8%;  Pred. No. 3.3e-08;
  Matches   49;  Conservative   28;  Mismatches   62;  Indels   20;  Gaps    7;

Qy          8 PSDXP-------VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              || :|       |||:   | :    |:| :     || :||: :   ||:   ||| :|
Db        133 PSPPPEKKEQRKVAHLTGKPNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVY 191

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
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              |:| |:|| |  |:: |:| :      | | :| :   ::| |         : |
Db        192 SKVYFRGQSC--TNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-------TTGQMWAHSS 242

Qy        119 YLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||| || | : | |   ::    ::| || | :||:  |
Db        243 YLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 280


RESULT 145
TNFL6_MACNE
ID   TNFL6_MACNE    STANDARD;      PRT;   280 AA.
AC   P63306; Q9BDM5; Q9MYL6;
DT   11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT   11-OCT-2004, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (CD95L protein) [Contains: Tumor necrosis
DE   factor ligand superfamily member 6, membrane form; Tumor necrosis
DE   factor ligand superfamily member 6, soluble form].
GN   Name=FASLG; Synonyms=CD95L, FASL, TNFSF6;
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9545;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   PubMed=12957408; DOI=10.1016/S0022-1759(03)00187-X;
RA   Kirii Y., Inoue T., Yoshino K., Kayagaki N., Yagita H., Okumura K.,
RA   Shibata H., Yoshikawa Y., Terao K.;
RT   "Molecular cloning, functional characterization, and enzyme-linked
RT   immunosorbent assay of cynomolgus monkey Fas ligand.";
RL   J. Immunol. Methods 278:201-209(2003).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Potential).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB035140; BAA90296.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    280       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034506.
FT   CHAIN       129    280       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000034507.
FT   TOPO_DOM      1     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    101       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    102    280       Extracellular (Potential).
FT   COMPBIAS      4     69       Pro-rich.
FT   COMPBIAS     45     64       Poly-Pro.
FT   SITE        128    129       Cleavage (By similarity).
FT   CARBOHYD    183    183       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    249    249       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    259    259       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    201    232       Potential.
SQ   SEQUENCE   280 AA;  31368 MW;  F0B284D61A132EB4 CRC64;

  Query Match             22.4%;  Score 176;  DB 1;  Length 280;
  Best Local Similarity   30.8%;  Pred. No. 3.3e-08;
  Matches   49;  Conservative   28;  Mismatches   62;  Indels   20;  Gaps    7;

Qy          8 PSDXP-------VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              || :|       |||:   | :    |:| :     || :||: :   ||:   ||| :|
Db        133 PSPPPEKKEQRKVAHLTGKPNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVY 191

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
              |:| |:|| |  |:: |:| :      | | :| :   ::| |          : |
Db        192 SKVYFRGQSC--TNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-------TTGQMWAHSS 242

Qy        119 YLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||| || | : | |   ::    ::| || | :||:  |
Db        243 YLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 280


RESULT 146
TNFC_PANTR
ID   TNFC_PANTR     STANDARD;      PRT;   244 AA.
AC   Q862Z7;
DT   21-NOV-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 25.
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   Name=LTB; Synonyms=TNFC, TNFSF3;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=22381002; PubMed=12493009;
RX   DOI=10.1034/j.1600-065X.2002.19008.x;
RA   Kulski J.K., Shiina T., Anzai T., Kohara S., Inoko H.;
RT   "Comparative genomic analysis of the MHC: the evolution of class I
RT   duplication blocks, diversity and complexity from shark to man.";
RL   Immunol. Rev. 190:95-122(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;
RA   Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA   Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA   Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA   Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT   "Comparative sequencing of human and chimpanzee MHC class I regions
RT   unveils insertions/deletions as the major path to genomic
RT   divergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface (By similarity).
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Potential).
```

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CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB054536; BAB83881.1; -; Genomic_DNA.
DR   EMBL; BA000041; BAC78156.1; -; Genomic_DNA.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    244       Lymphotoxin-beta.
FT                                /FTId=PRO_0000185491.
FT   TOPO_DOM      1     18       Cytoplasmic (Potential).
FT   TRANSMEM     19     48       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     49    244       Extracellular (Potential).
FT   CARBOHYD    222    222       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   244 AA;  25420 MW;  A4047858335D5B97 CRC64;

  Query Match             22.3%;  Score 175;  DB 1;  Length 244;
  Best Local Similarity   26.2%;  Pred. No. 3.4e-08;
  Matches   42;  Conservative   34;  Mismatches   64;  Indels   20;  Gaps    5;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ-LVVPSEGLYLIYSQVLFXGQGC 69
              :| ||::  |      | |   :  | | :| :  | : | :| :||| :|  | ::|:
Db         87 LPAAHLIGAPLKGQGLGWETTKEQAFLTSGTQFSDAEGLALPQDGLYYLYCLVGYRGRTP 146

Qy         70 P------STHVLLTHTISRIAVSY--------QTXVNLLSAIXSPCQRETPEGAEAXPWY 115
              |         | |  :: |   :|          :   :: :: | :|:       : ||
Db        147 PGGGDPQGRSVTLRSSLYRAGGAYGPGTPELLLEGAETVTPVLDPARRQ----GYGPLWY 202

Qy        116 EPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
                :  ||: || :|:|:   |: || :|||  |: :|| :
Db        203 TSVGFGGLVQLRRGERVYVNISHPDMVDFAR-GKTFFGAV 241


RESULT 147
Q6J0S0_PERLE
ID   Q6J0S0_PERLE   PRELIMINARY;   PRT;   112 AA.
AC   Q6J0S0;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Tumor necrosis factor (Fragment).
OS   Peromyscus leucopus (White-footed mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Neotominae; Peromyscus.
OX   NCBI_TaxID=10041;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pyter L.M., Hotchkiss A.K., Nelson R.J.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY608911; AAT44329.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  12278 MW;  3866EAB86C0ABAC1 CRC64;

  Query Match             22.1%;  Score 174;  DB 2;  Length 112;
  Best Local Similarity   70.2%;  Pred. No. 1.5e-08;
  Matches   33;  Conservative    9;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ 47
              :||||:  ||:||||||||| | : ||:||:||||||||||::|:|||
Db         66 LRSSSQNSSDKPVAHVVANHQVDEQLEWLSRRANALLANGMDLKDNQ 112


RESULT 148
TNFC_MACMU
ID   TNFC_MACMU     STANDARD;      PRT;   244 AA.
AC   Q5TM22;
DT   16-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT   21-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   Name=LTB; Synonyms=TNFC, TNFSF3;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15269276; DOI=10.1093/molbev/msh216;
RA   Kulski J.K., Anzai T., Shiina T., Inoko H.;
RT   "Rhesus macaque class I duplicon structures, organization, and
RT   evolution within the alpha block of the major histocompatibility
RT   complex.";
RL   Mol. Biol. Evol. 21:2079-2091(2004).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface (By similarity).
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB128049; BAD69723.1; -; Genomic_DNA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    244       Lymphotoxin-beta.
FT                                /FTId=PRO_0000185488.
FT   TOPO_DOM      1     18       Cytoplasmic (Potential).
FT   TRANSMEM     19     48       Signal-anchor for type II membrane
FT                                protein (Potential).
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FT   TOPO_DOM     49    244       Extracellular (Potential).
FT   CARBOHYD    222    222       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   244 AA;  25259 MW;  46AA5DEEE255B6C2 CRC64;

  Query Match             22.1%;  Score 174;  DB 1;  Length 244;
  Best Local Similarity   28.8%;  Pred. No. 4.2e-08;
  Matches   45;  Conservative   31;  Mismatches   68;  Indels   12;  Gaps    5;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRD-NQLVVPSEGLYLIYSQVLFXGQGC 69
              :| ||:: |     | |   :  | | :| :  | : | :| :||| :|  | ::|:
Db         87 LPAAHLIGAPLKGQGLGWEATKEQAFLTSGTQFSDADGLALPQDGLYYLYCLVGYRGRAP 146

Qy         70 P------STHVLLTHTISRIAVSY--QTXVNLLSAIXSPCQRETPEGAEAXP--WYEPIY 119
              |      | |  :: |   :|   |:  ||   ::      | | : :   ||  :
Db        147 PGGAEPRGRSVTLRSSLYRAGGAYGPGTPELLLEGAETVTPVLDPAGRQGYGPLWYTSVG 206

Qy        120 LGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
               ||: || :|:|:   |: || :|||  |: :|| :
Db        207 FGGLVQLRRGERVYVNISHPDMVDFAR-GKTFFGAV 241


RESULT 149
TNFL6_CERTO
ID   TNFL6_CERTO    STANDARD;      PRT;   280 AA.
AC   Q9BDN1;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 32.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (Protein CD95L) [Contains: Tumor necrosis
DE   factor ligand superfamily member 6, membrane form; Tumor necrosis
DE   factor ligand superfamily member 6, soluble form].
GN   Name=FASLG; Synonyms=CD95L, FASL, TNFSF6;
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lymphocyte;
RX   MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA   Villinger F.J., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF344847; AAK37606.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    280       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034498.
FT   CHAIN       129    280       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000034499.
FT   TOPO_DOM      1     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    101       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    102    280       Extracellular (Potential).
FT   COMPBIAS      4     69       Pro-rich.
FT   COMPBIAS     45     64       Poly-Pro.
FT   SITE        128    129       Cleavage (By similarity).
FT   CARBOHYD    183    183       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    249    249       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    259    259       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    201    232       Potential.
SQ   SEQUENCE   280 AA;  31408 MW;  729EA60067B7D398 CRC64;

  Query Match             22.1%;  Score 174;  DB 1;  Length 280;
  Best Local Similarity   30.8%;  Pred. No. 5.1e-08;
  Matches   49;  Conservative   28;  Mismatches   62;  Indels   20;  Gaps    7;

Qy          8 PSDXP-------VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              || :|       |||:   | :    |:| :     || :||: :   ||:   ||| :|
Db        133 PSPPPEKKEQRKVAHLTGKPNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVY 191

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
              |:| |:|| |  |:: |:| :       | | :| :   ::| |             : |
Db        192 SKVYFRGQSC--TNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-------TTGQMWAHSS 242

Qy        119 YLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||| || | : | |   ::    ::| || | :||:  |
Db        243 YLGAVFNLTSTDHLYVNVSELSLVNFEES-QTFFGLYKL 280


RESULT 150
TNFL6_MOUSE
ID   TNFL6_MOUSE    STANDARD;      PRT;   279 AA.
AC   P41047; Q61217; Q9R1F2;
DT   01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1995, sequence version 1.
DT   07-FEB-2006, entry version 63.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (CD95L protein) [Contains: Tumor necrosis
DE   factor ligand superfamily member 6, membrane form; Tumor necrosis
DE   factor ligand superfamily member 6, soluble form].
GN   Name=Faslg; Synonyms=Aptl1g1, Fasl, gld, Tnfsf6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM FASL).
RX   MEDLINE=94185175; PubMed=7511063; DOI=10.1016/0092-8674(94)90375-1;
RA   Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA   Suda T., Nagata S.;
RT   "Generalized lymphoproliferative disease in mice, caused by a point
RT   mutation in the Fas ligand.";
RL   Cell 76:969-976(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC   STRAIN=C57BL/6;
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RX   MEDLINE=95388076; PubMed=7544870; DOI=10.1016/0161-5890(95)00016-8;
RA   Peitsch M.C., Tschopp J.;
RT   "Comparative molecular modelling of the Fas-ligand and other members
RT   of the TNF family.";
RL   Mol. Immunol. 32:761-772(1995).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM FASL).
RX   MEDLINE=95196085; PubMed=7889405; DOI=10.1016/1074-7613(94)90106-6;
RA   Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA   Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT   "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF
RT   family gene cluster.";
RL   Immunity 1:131-136(1994).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM FASL).
RC   STRAIN=BALB/c;
RA   Fenner M.H., Shioda T., Isselbacher K.J.;
RT   "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two
RT   amino acids.";
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM FASLS).
RC   STRAIN=C3H; TISSUE=Spleen;
RX   MEDLINE=20021694; PubMed=10552956;
RA   Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
RA   Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
RT   "Cloning and expression of a short Fas ligand: a new alternatively
RT   spliced product of the mouse Fas ligand gene.";
RL   Blood 94:3456-3467(1999).
RN   [6]
RP   CHARACTERIZATION OF VARIANT GLD.
RX   MEDLINE=96091792; PubMed=7495745;
RA   Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
RA   Rousseau M., Bron C., Renno T., French L., Tschopp J.;
RT   "Characterization of the non-functional Fas ligand of gld mice.";
RL   Int. Immunol. 7:1381-1386(1995).
RN   [7]
RP   VARIANTS ALA-184 AND GLY-218.
RC   STRAIN=BALB/c, C3H, C57BL/6, DBA/1, DBA/2, MRL, NOD, NZB, NZW, and
RC   SJL;
RX   MEDLINE=97268671; PubMed=9108079; DOI=10.1073/pnas.94.8.3914;
RA   Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
RA   Yagita H.;
RT   "Polymorphism of murine Fas ligand that affects the biological
RT   activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
CC       Secreted (isoforms FASL and FASLS).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=FasL;
CC         IsoId=P41047-1; Sequence=Displayed;
CC       Name=FasLS;
CC         IsoId=P41047-2; Sequence=VSP_006445;
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- DISEASE: A deficiency in this protein is the cause of generalized
CC       lymphoproliferation disease phenotype (gld). Gld mice present
CC       lymphadenopathy and autoantibody production. The phenotype is
CC       recessively inherited.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U06948; AAA17800.1; -; mRNA.
DR   EMBL; U10984; AAA19778.1; -; mRNA.
DR   EMBL; S76752; AAB33780.1; -; mRNA.
DR   EMBL; U58995; AAB02915.1; -; mRNA.
DR   EMBL; AF119335; AAD52106.1; -; mRNA.
DR   PIR; A53062; A53062.
DR   HSSP; P50591; 1DG6.
DR   Ensembl; ENSMUSG00000000817; Mus musculus.
DR   MGI; MGI:99255; Fasl.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0046666; P:retinal cell programmed cell death; IMP.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Alternative splicing; Apoptosis; Cytokine; Disease mutation;
KW   Glycoprotein; Membrane; Polymorphism; Signal-anchor; Transmembrane.
FT   CHAIN         1    279       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034508.
FT   CHAIN       128    279       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000034509.
FT   TOPO_DOM      1     78       Cytoplasmic (Potential).
FT   TRANSMEM     79    100       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    101    279       Extracellular (Potential).
FT   COMPBIAS      4     69       Pro-rich.
FT   COMPBIAS     45     51       Poly-Pro.
FT   SITE        127    128       Cleavage (By similarity).
FT   CARBOHYD    117    117       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    182    182       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    248    248       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    258    258       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    200    231       Potential.
FT   VARSPLIC      1    210       Missing (in isoform FasLS).
FT                                /FTId=VSP_006445.
FT   VARIANT     184    184       T -> A (in strain: BALB/c, DBA/1 and DBA/
FT                                2; enhances cytotoxicity).
FT   VARIANT     218    218       E -> G (in strain: BALB/c, DBA/1 and DBA/
FT                                2; enhances cytotoxicity).
FT   VARIANT     273    273       F -> L (in gld; abolishes binding of FASL
FT                                to its receptor).
SQ   SEQUENCE   279 AA;  31442 MW;  37972E2728E0A1CA CRC64;

  Query Match             21.6%;  Score 169.5;  DB 1;  Length 279;
  Best Local Similarity   29.5%;  Pred. No. 1.4e-07;
  Matches   46;  Conservative   30;  Mismatches   65;  Indels   15;  Gaps    6;

Qy          7 TPSD----XPVAHVVANPQAEG-QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
              |||:    : |||:  || :    |:| :    ||: :||: :   ||:   ||| :||:
Db        134 TPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTALI-SGVKYKKGGLVINETGLYFVYSK 192

Qy         62 VLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLG 121
              | |:|| |   :  | | :      |  :: |:       ::        : |    |||
Db        193 VYFRGQSC--NNQPLNHKVYMRNSKYPEDLVLME------EKRLNYCTTGQIWAHSSYLG 244

Qy        122 GVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               || | : | |   |::   ::| || : :||:  |
Db        245 AVFNLTSADHLYVNISQLSLINFEES-KTFFGLYKL 279


RESULT 151
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Q544E9_MOUSE
ID   Q544E9_MOUSE   PRELIMINARY;   PRT;   279 AA.
AC   Q544E9;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   0 day neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A430069F14 product:tumor necrosis factor (ligand) superfamily,
DE   member 6, full insert sequence (7 days embryo whole body cDNA, RIKEN
DE   full-length enriched library, clone:C430011C24 product:tumor necrosis
DE   factor (ligand) superfamily, member 6, full insert sequence).
GN   Name=Fasl;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus, and Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus, and Whole body;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus, and Whole body;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus, and Whole body;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus, and Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus, and Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus, and Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK040139; BAC30520.1; -; mRNA.
DR   EMBL; AK141268; BAE24625.1; -; mRNA.
DR   Ensembl; ENSMUSG00000000817; Mus musculus.
DR   MGI; MGI:99255; Fasl.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   GO; GO:0046666; P:retinal cell programmed cell death; IMP.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.

  Query Match             21.6%;  Score 169.5;  DB 2;  Length 279;
  Best Local Similarity   29.5%;  Pred. No. 1.4e-07;
  Matches   46;  Conservative   30;  Mismatches   65;  Indels   15;  Gaps    6;

Qy          7 TPSD----XPVAHVVANPQAEG-QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
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Db        134 TPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTALI-SGVKYKKGGLVINETGLYFVYSK 192

Qy         62 VLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLG 121
              | |:|| |   :  | | :     |  :: |:      ::       : |    |||
Db        193 VYFRGQSC--NNQPLNHKVYMRNSKYPEDLVLME------EKRLNYCTTGQIWAHSSYLG 244

Qy        122 GVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                || | : | |   |::   ::| || : :||:  |
Db        245 AVFNLTSADHLYVNISQLSLINFEES-KTFFGLYKL 279
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RESULT 152
Q7TMV9_MOUSE
ID   Q7TMV9_MOUSE   PRELIMINARY;   PRT;   279 AA.
AC   Q7TMV9;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Fasl protein.
GN   Name=Fasl;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RG   NIH MGC Project;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC052866; AAH52866.1; -; mRNA.
DR   HSSP; P50591; 1DG6.
DR   Ensembl; ENSMUSG00000000817; Mus musculus.
DR   MGI; MGI:99255; Fasl.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   GO; GO:0046666; P:retinal cell programmed cell death; IMP.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   279 AA;  31416 MW;  C2972E2728FBBB7B CRC64;

  Query Match             20.9%;  Score 164.5;  DB 2;  Length 279;
  Best Local Similarity   28.8%;  Pred. No. 4.2e-07;
  Matches   45;  Conservative   31;  Mismatches   65;  Indels   15;  Gaps    6;
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Qy          7 TPSD----XPVAHVVANPQAEG-QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
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Db        134 TPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTALI-SGVKYKKGGLVINETGLYFVYSK 192

Qy         62 VLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLG 121
              | |:|| |   :  | | :      |  :: |:       ::        : |    :||
Db        193 VYFRGQSC--NNQPLNHKVYMRNSKYPEDLVLME------EKRLNYCTTGQIWAHSSHLG 244

Qy        122 GVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                || | : | |   |::   ::| || : :||:  |
Db        245 AVFNLTSADHLYVNISQLSLINFEES-KTFFGLYKL 279


RESULT 153
TNF14_MOUSE
ID   TNF14_MOUSE    STANDARD;      PRT;   239 AA.
AC   Q9QYH9;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 39.
DE   Tumor necrosis factor ligand superfamily member 14 (CD258 antigen)
DE   [Contains: Tumor necrosis factor ligand superfamily member 14,
DE   membrane form; Tumor necrosis factor ligand superfamily member 14,
DE   soluble form].
GN   Name=Tnfsf14; Synonyms=Light;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=20165223; PubMed=10700230; DOI=10.1038/73136;
RA   Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., Flies D.,
RA   Boone T., Hsu H., Fu Y.-X., Nagata S., Ni J., Chen L.;
RT   "Modulation of T-cell-mediated immunity in tumor and graft-versus-host
RT   disease models through the LIGHT co-stimulatory pathway.";
RL   Nat. Med. 6:283-289(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Fetal liver;
RX   MEDLINE=20354998; PubMed=10894944;
RA   Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;
RT   "Molecular cloning and characterization of a mouse homolog of human
RT   TNFSF14, a member of the TNF superfamily.";
RL   Cytogenet. Cell Genet. 89:89-91(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lymphoma;
RA   Force W.R., Todd P.K., Mikayama T.;
RT   "Mouse LIGHT; molecular genetics, ligand binding and expression.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
CC       decoy receptor TNFRSF6B modulates its effects. Activates NFKB and
CC       stimulates the proliferation of T cells.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF123385; AAF76453.1; -; mRNA.
DR   EMBL; AB029155; BAA88559.1; -; mRNA.
DR   EMBL; AF227533; AAF36722.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   Ensembl; ENSMUSG00000005824; Mus musculus.
DR   MGI; MGI:1355317; Tnfsf14.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0043027; F:caspase inhibitor activity; ISS.
DR   GO; GO:0005102; F:receptor binding; ISS.
DR   GO; GO:0001719; P:inhibition of caspase activation; ISS.
DR   GO; GO:0008588; P:release of cytoplasmic sequestered NF-kappaB; ISS.
DR   GO; GO:0007165; P:signal transduction; ISS.
DR   GO; GO:0043029; P:T cell homeostasis; ISS.
DR   GO; GO:0042098; P:T cell proliferation; ISS.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    239       Tumor necrosis factor ligand superfamily
FT                                member 14, membrane form.
FT                                /FTId=PRO_0000034534.
FT   CHAIN       ?82    239       Tumor necrosis factor ligand superfamily
FT                                member 14, soluble form.
FT                                /FTId=PRO_0000034535.
FT   TOPO_DOM      1     37       Cytoplasmic (Potential).
FT   TRANSMEM     38     58       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     59    239       Extracellular (Potential).
FT   SITE         81     82       Cleavage (Potential).
FT   CARBOHYD    100    100       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    191    191       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    152    187       Potential.
SQ   SEQUENCE   239 AA;  26338 MW;  217874AC71AD6BE3 CRC64;

  Query Match             20.7%;  Score 163;  DB 1;  Length 239;
  Best Local Similarity   29.0%;  Pred. No. 4.7e-07;
  Matches   45;  Conservative   28;  Mismatches   70;  Indels   12;  Gaps    5;

Qy          6 RTPSDXPVAHVV-ANPQ---AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
              |:   :| ||:  ||       | | |  |  | |  |:  |  ||   | | :||:
Db         86 RSHQANPAAHLTGANASLIGIGGPLLWETRLGLAFL-RGLTYHDGALVTMEPGYYYVYSK 144

Qy         62 VLFXGQGCP---STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
              |  :| |||   :  : :|| : :   |  :: || : :||| |       :: |::
Db        145 VQLSGVGCPQGLANGLPITHGLYKRTSRYPKELELLVSRRSPCGRAN----SSRVWWDSS 200

Qy        119 YLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
              :||||  ||:|: :   :     :   :  : |||
Db        201 FLGGVVHLEAGEEVVVRVPGNRLVRPRDGTRSYFG 235


RESULT 154
TNFL6_HUMAN
ID   TNFL6_HUMAN    STANDARD;      PRT;   281 AA.
AC   P48023; Q9BZP9;
DT   01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1996, sequence version 1.
DT   07-MAR-2006, entry version 62.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (CD95L protein) (Apoptosis antigen
DE   ligand) (APTL) [Contains: Tumor necrosis factor ligand superfamily
DE   member 6, membrane form; Tumor necrosis factor ligand superfamily
DE   member 6, soluble form].
GN   Name=FASLG; Synonyms=APT1LG1, FASL, TNFSF6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX   MEDLINE=95105731; PubMed=7528780; DOI=10.1084/jem.181.1.71;
RA   Alderson M.;
RT   "Fas ligand mediates activation-induced cell death in human T
```

```
RT   lymphocytes.";
RL   J. Exp. Med. 181:71-77(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX   MEDLINE=95127560; PubMed=7826947;
RA   Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT   "Human Fas ligand: gene structure, chromosomal location and species
RT   specificity.";
RL   Int. Immunol. 6:1567-1574(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA   Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX   MEDLINE=95071350; PubMed=7980502;
RA   Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RA   Fusamoto H., Kamada T.;
RT   "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT   infection.";
RL   Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RC   TISSUE=Leukocyte;
RA   Zeytun A., Nagarkatti M., Nagarkatti P.S.;
RT   "Isolation and characterization of a new naturally occuring variant of
RT   human Fas ligand that is expressed only in membrane bound form.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG   Human chromosome 1 international sequencing consortium;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Blood;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.
RC   TISSUE=Blood;
RA   Matsumura M., Nakanishi Y., Ohba Y.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX   MEDLINE=97373583; PubMed=9228058; DOI=10.1074/jbc.272.30.18827;
RA   Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
RA   Terskikh A., Peitsch M.C., Tschopp J.;
RT   "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL   J. Biol. Chem. 272:18827-18833(1997).
RN   [10]
RP   PROCESSING.
RX   MEDLINE=98087475; PubMed=9427603; DOI=10.1038/nm0198-031;
RA   Tanaka M., Itai T., Adachi M., Nagata S.;
RT   "Downregulation of Fas ligand by shedding.";
RL   Nat. Med. 4:31-36(1998).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects.
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released
CC       into the extracellular fluid, probably by cleavage form the cell
CC       surface.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P48023-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P48023-2; Sequence=VSP_006443, VSP_006444;
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing.
CC   -!- DISEASE: Defects in FASLG are a cause of autoimmune
CC       lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
CC       Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
CC       involving hemolytic anemia and thrombocytopenia with massive
CC       lymphadenopathy and splenomegaly.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U08137; AAC50071.1; -; mRNA.
DR   EMBL; U11821; AAC50124.1; -; mRNA.
DR   EMBL; X89102; CAA61474.1; -; mRNA.
DR   EMBL; D38122; BAA07320.1; -; mRNA.
DR   EMBL; AF288573; AAG60017.1; -; mRNA.
DR   EMBL; Z96050; CAB09424.1; -; Genomic_DNA.
DR   EMBL; BC017502; AAH17502.1; -; mRNA.
DR   EMBL; AB013303; BAA32542.1; -; Genomic_DNA.
DR   PIR; I38707; I38707.
DR   PDB; 1BZI; Model; B/C=1-281.
DR   IntAct; P48023; -.
DR   Ensembl; ENSG00000117560; Homo sapiens.
DR   H-InvDB; HIX0001337; -.
DR   HGNC; HGNC:11936; FASLG.
DR   MIM; 134638; gene.
DR   MIM; 601859; phenotype.
DR   Reactome; P48023; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0006917; P:induction of apoptosis; TAS.
DR   GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   3D-structure; Alternative splicing; Antigen; Apoptosis; Cytokine;
KW   Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    281       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034500.
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FT   CHAIN       130    281       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form.
FT                                /FTId=PRO_0000034501.
FT   TOPO_DOM      1     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    102       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     103    281      Extracellular (Potential).
FT   COMPBIAS      4     70       Pro-rich.
FT   COMPBIAS     45     65       Poly-Pro.
FT   SITE        129    130       Cleavage.
FT   CARBOHYD    184    184       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    250    250       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    260    260       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    202    233       Potential.
FT   VARSPLIC    117    127       STSQMHTASSL -> ATPVHPLKKRS (in isoform
FT                                2).
FT                                /FTId=VSP_006443.
FT   VARSPLIC    128    281       Missing (In isoform 2).
FT                                /FTId=VSP_006444.
FT   MUTAGEN     206    206       P->D,F,R: Lowers binding to TNFRSF6 and
FT                                reduces cytotoxity more than 100-fold.
FT   MUTAGEN     218    218       Y->F,R: Lowers binding to TNFRSF6 and
FT                                abolishes cytotoxity.
FT   MUTAGEN     275    275       F->L: Abolishes binding to TNRFSF6 and
FT                                cytotoxicity.
FT   STRAND      146    148
FT   STRAND      169    169
FT   STRAND      175    177
FT   TURN        178    179
FT   STRAND      180    182
FT   STRAND      184    185
FT   STRAND      187    191
FT   STRAND      194    198

  Query Match             20.7%;  Score 163;  DB 1;  Length 281;
  Best Local Similarity   29.6%;  Pred. No. 5.9e-07;
  Matches   47;  Conservative   28;  Mismatches   64;  Indels   20;  Gaps    7;

Qy          8 PSDXP-------VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              || :|       |||:     :    |:| :     || :||: :   ||:   ||| :|
Db        134 PSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVY 192

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
              |:| |:|| |   :: |:| :      | | :| :   ::| |         : |
Db        193 SKVYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-------TTGQMWARSS 243

Qy        119 YLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||| || | : | |   ::    ::| || | :||:  |
Db        244 YLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 281


RESULT 155
Q53ZZ1_HUMAN
ID   Q53ZZ1_HUMAN   PRELIMINARY;   PRT;   281 AA.
AC   Q53ZZ1;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   FAS ligand.
GN   Name=FASLG; Synonyms=TNFSF6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   He X., Xu L., Liu Y., Zeng Y.;
RT   "Cloning and polymorphism analysis of FasL.";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY225406; AAO43991.1; -; mRNA.
DR   Ensembl; ENSG00000117560; Homo sapiens.
DR   HGNC; HGNC:11936; FASLG.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   281 AA;  31485 MW;  A8A6EB358246E9BB CRC64;

  Query Match             20.7%;  Score 163;  DB 2;  Length 281;
  Best Local Similarity   29.6%;  Pred. No. 5.9e-07;
  Matches   47;  Conservative   28;  Mismatches   64;  Indels   20;  Gaps    7;

Qy          8 PSDXP-------VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              || :|       |||:     :    |:| :     || :||: :   ||:   ||| :|
Db        134 PSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVY 192

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
              |:| |:|| |   :: |:| :      | | :| :   ::| |         : |
Db        193 SKVYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-------TTGQMWARSS 243

Qy        119 YLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||| || | : | |   ::    ::| || | :||:  |
Db        244 YLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 281


RESULT 156
Q7T2Q3_CYPCA
ID   Q7T2Q3_CYPCA   PRELIMINARY;   PRT;   227 AA.
AC   Q7T2Q3;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Tumor necrosis factor-3 alpha.
GN   Name=TNF-3alpha;
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Head kidney;
RX   PubMed=15145420; DOI=10.1016/j.fsi.2003.11.001;
RA   Savan R., Sakai M.;
RT   "Presence of multiple isoforms of TNF alpha in carp (Cyprinus carpio
RT   L.): genomic and expression analysis.";
RL   Fish Shellfish Immunol. 17:87-94(2004).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB112424; BAC77690.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
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DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   227 AA;  25227 MW;  010BC2B1E8D7265E CRC64;

  Query Match             20.7%;  Score 162.5;  DB 2;  Length 227;
  Best Local Similarity   25.5%;  Pred. No. 4.9e-07;
  Matches   38;  Conservative   37;  Mismatches   51;  Indels   23;  Gaps    6;

Qy         22 AEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPS--------TH 73
              ::  : |    :  | :: |::| | ::::|::|:| ||||| |:   | :         |
Db         89 SKNNIDWKQNQDGAFVSGGLKLVDREIIIPNDGIYFIYSQVSFH-ISCKNDMTEDQEVMH 147

Qy         74 VLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLS 133
              |  :| :   :  :   :  |: | :| |   :      : ||: |||| | | :||:|
Db        148 V--SHAVFHYSDFFGIYKPLIRAARSACVHAS---NTEDVWYDTIYLGAAFSLRAGDKLC 202

Qy        134 AE-----INRPDYLDFAESGQVYFGIIAL 157
               :     : | :     :: : :||: ||
Db        203 TKTTTELLPRVE----TDNAKTFFGVFAL 227


RESULT 157
TNFC_MARMO
ID   TNFC_MARMO     STANDARD;      PRT;   310 AA.
AC   Q9JMI0; Q9JM11;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2000, sequence version 1.
DT   07-FEB-2006, entry version 31.
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   Name=LTB; Synonyms=TNFC, TNFSF3;
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Sciuridae; Xerinae; Marmotini; Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20184748; PubMed=10721723; DOI=10.1016/S0378-1119(99)00494-1;
RA   Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
RT   "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis factor genes:
RT   structure, characterization and biological activity.";
RL   Gene 242:295-305(2000).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF096268; AAF34866.1; -; Genomic_DNA.
DR   EMBL; AF095587; AAF34865.1; -; mRNA.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    310       Lymphotoxin-beta.
FT                                /FTId=PRO_0000185489.
FT   TOPO_DOM      1     27       Cytoplasmic (Potential).
FT   TRANSMEM     28     48       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     49    310       Extracellular (Potential).
FT   CARBOHYD    272    272       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    280    280       D -> H (in Ref. 1; AAF34865).
SQ   SEQUENCE   310 AA;  32644 MW;  73B354EFC8B3B3BE CRC64;

  Query Match             20.5%;  Score 161;  DB 1;  Length 310;
  Best Local Similarity   25.3%;  Pred. No. 1e-06;
  Matches   42;  Conservative   33;  Mismatches   63;  Indels   28;  Gaps    5;

Qy          9 SDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ-LVVPSEGLYLIYSQVLFXGQ 67
              | :| ||::          | |  ::  | | :| :    : | :| :||| :|  | ::|:
Db        135 SRLPAAHLIGAWMKGQGLSWEAKKEEAFLRSGTQFSGAEGLALPQDGLYYLYCNVGYRGR 194

Qy         68 GCPS------THVLLTHTISRIAVSY-----------QTXVNLLSAIXSPCQRETPEGA 109
              ||        | |  :: |   :|            :|:  :|   : | |
Db        195 APPSGAGPQDRSVTLRSSLYRAGGAYGRGAPELLLEGAETVTPVLDRAGRPQYR------ 248

Qy        110 EAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
                : ||  :  ||: || :|:|:   |: || :|:   |: :|| :
Db        249 --PLWYTSVGFGGLVQLRRGERVYVNISHPDMVDY-RRGKTFFGAV 291


RESULT 158
TNFL6_PIG
ID   TNFL6_PIG      STANDARD;      PRT;   282 AA.
AC   Q9BEA8; Q95M04; Q95N10;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2001, sequence version 1.
DT   21-FEB-2006, entry version 33.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) (CD95L protein) [Contains: Tumor necrosis
DE   factor ligand superfamily member 6, membrane form; Tumor necrosis
DE   factor ligand superfamily member 6, soluble form].
GN   Name=FASLG; Synonyms=FASL, TNFSF6;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21322533; PubMed=11429161; DOI=10.1089/107999001300177493;
RA   Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
RT   "Molecular cloning, characterization, and expression of porcine Fas
RT   ligand (CD95 ligand).";
RL   J. Interferon Cytokine Res. 21:305-312(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Guanxi bama miniature pig;
RA   Zhu N., Young Y.;
RT   "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymphoid;
RA   Tsuyuki S., Kono M., Bloom E.T.;
RT   "Cloning and potential utility of porcine Fas ligand: overexpression
RT   in porcine cells protects them from attack by human cytolytic cells.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Landrace X Large Yorkshire white; TISSUE=Thymocyte;
```

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RX   MEDLINE=21653191; PubMed=11792426; DOI=10.1016/S0161-5890(01)00098-0;
RA   Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;
RT   "Porcine Fas-ligand gene: genomic sequence analysis and comparison
RT   with human gene.";
RL   Mol. Immunol. 38:581-586(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- INDUCTION: By IL-18.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB027297; BAB40919.1; -; mRNA.
DR   EMBL; AY033634; AAK56449.1; -; mRNA.
DR   EMBL; AF397407; AAK84408.1; -; mRNA.
DR   EMBL; AB069764; BAB64291.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    282       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000034510.
FT   CHAIN       131    282       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000034511.
FT   TOPO_DOM      1     82       Cytoplasmic (Potential).
FT   TRANSMEM     83    103       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    104    282       Extracellular (Potential).
FT   COMPBIAS      4     70       Pro-rich.
FT   COMPBIAS     45     56       Poly-Pro.
FT   SITE        130    131       Cleavage (By similarity).
FT   CARBOHYD    185    185       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    251    251       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    261    261       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    203    234       Potential.
FT   CONFLICT      5      5       F -> L (in Ref. 4).
FT   CONFLICT     57     57       T -> P (in Ref. 2).
SQ   SEQUENCE   282 AA;  31756 MW;  6743DAA1145671FB CRC64;

  Query Match             19.9%;  Score 156.5;  DB 1;  Length 282;
  Best Local Similarity   29.7%;  Pred. No. 2.5e-06;
  Matches   47;  Conservative   29;  Mismatches   61;  Indels   21;  Gaps    8;

Qy          8 PSD----XPVAHVVANPQAEG-QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 62
              ||:    : |||:   | :    |:| :    ||: :||:     ||:   ||| :||:|
Db        138 PSEKKELRKVAHLTGKPNSRSIPLEWEDTYGIALV-SGVKYMKGSLVINDTGLYFVYSKV 196

Qy         63 LFXGQGC---PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIY 119
              |:|| |   | :| : |   ||     | :| :   ::: |          : |    |
Db        197 YFRGQYCNNQPLSHKVYTRN-SRYP---QDLVLMEGKMMNYC-------TTGQMWARSSY 245

Qy        120 LGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              || || | : | |   ::    ::| || : :||:  |
Db        246 LGAVFNLTSADHLYVNVSELSLVNFEES-KTFFGLYKL 282


RESULT 159
Q2TPW2_CTEID
ID   Q2TPW2_CTEID   PRELIMINARY;   PRT;   299 AA.
AC   Q2TPW2;
DT   24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   24-JAN-2006, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   TNF-related apoptosis inducing ligand TRAIL.
OS   Ctenopharyngodon idella (Grass carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Ctenopharyngodon.
OX   NCBI_TaxID=7959;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Chang M.X., Nie P.;
RT   "Cloning of grass carp tumor necrosis factor related apoptosis
RT   inducing ligand gene and its expression in Escherichia coli.";
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY697730; AAW22593.1; -; mRNA.
DR   EMBL; AY697729; AAW22592.1; -; Genomic_DNA.
SQ   SEQUENCE   299 AA;  33330 MW;  BFED80955C139C1E CRC64;

  Query Match             19.9%;  Score 156.5;  DB 2;  Length 299;
  Best Local Similarity   28.3%;  Pred. No. 2.7e-06;
  Matches   54;  Conservative   29;  Mismatches   57;  Indels   51;  Gaps   11;

Qy          1 VRSSSRTPSDXPVAHVVAN--PQAE-----------GQ--LQWLNRRANALLANGVELR 44
              ::    :|  :  |||  :  |:||            ||    | : :  | | | |||
Db        117 IQDQDDSPRPKIAAHVTGSYIPEAEKDGGGLPNRKVYGQKIQSWESEKGLAFLQN-VELS 175

Qy         45 DNQLVVPSEGLYLIYSQVLF-----------------XGQ---GCPSTHVLLTHTISRI 83
              | :||||  ||| ||||  |                 :||   | |    :| :   ::
Db        176 DGELVVPQAGLYYIYSQTYFRHSLIEEDESDHGEEDGTSGQSVRGKP----MLQYVYKKV 231

Qy         84 AVSYQTXVNLLSAIXSPC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYL 142
              : ||  :: |:   :: |  |:|  |  :      ||  |:||| :|||:   ::    :
Db        232 S-SYPVPILLMKNARTTCWSRDTQYGLYS------IYQAGLFQLGGGDRVFVTVSNVSTI 284

Qy        143 DFAESGQVYFG 153
              |  |    :||
Db        285 DMDEKSS-FFG 294


RESULT 160
Q6MG45_RAT
ID   Q6MG45_RAT     PRELIMINARY;   PRT;   306 AA.
AC   Q6MG45;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Lymphotoxin beta (TNF superfamily, member 3) (Lymphotoxin B).
GN   Name=Ltb;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
```

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RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Brown Norway;
RX   PubMed=15060004; DOI=10.1101/gr.1987704;
RA   Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA   Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
RT   "The genomic sequence and comparative analysis of the rat major
RT   histocompatibility complex.";
RL   Genome Res. 14:631-639(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Brown Norway;
RA   Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
RA   Lang N., Lehrack S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
RA   Sudbrak R., Reinhardt R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RA   Director MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BX883046; CAE84002.1; -; Genomic_DNA.
DR   EMBL; BC088208; AAH88208.1; -; mRNA.
DR   Ensembl; ENSRNOG00000000836; Rattus norvegicus.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   306 AA;  32552 MW;  4871532A8E7AEA45 CRC64;

  Query Match             19.8%;  Score 156;  DB 2;  Length 306;
  Best Local Similarity   25.3%;  Pred. No. 3.1e-06;
  Matches   41;  Conservative   33;  Mismatches   62;  Indels   26;  Gaps    5;

Qy         10 DXPVAHVVANPQAEGQLQWLNRRANALLANGVEL-RDNQLVVPSEGLYLIYSQVLFXGQG 68
              ::| ||::    :   | |   :  | | :| :  | : | :| :|:| :|  | ::|:

Db        152 ELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSRTHGLALPQDGVYYLYCHVGYRGRT 211

Qy         69 CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP----EGAEAXP---------- 113
               |:          |      |: : |   :    | :|    |||| :
Db        212 PPA---------GRSRARLFTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSL 262

Qy        114 WYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
              ||  :  ||: || :|:|:   |: || :|:   |: :|| :
Db        263 WYTSVGFGGLAQLRSGERIYVNISHPDMVDY-RRGKTFFGAV 303


RESULT 161
Q7TSL5_PERMA
ID   Q7TSL5_PERMA   PRELIMINARY;   PRT;   302 AA.
AC   Q7TSL5;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Lymphotoxin beta.
GN   Name=LTB;
OS   Peromyscus maniculatus (Deer mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Neotominae; Peromyscus.
OX   NCBI_TaxID=10042;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hegg T.R., Schountz T.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY282503; AAP34710.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   302 AA;  31840 MW;  F28AE6229D2540BF CRC64;

  Query Match             19.7%;  Score 154.5;  DB 2;  Length 302;
  Best Local Similarity   25.3%;  Pred. No. 4.3e-06;
  Matches   41;  Conservative   33;  Mismatches   61;  Indels   27;  Gaps    6;

Qy         10 DXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ-LVVPSEGLYLIYSQVLFXGQG 68
              ::| ||::    | :| |   :  | | :||:      | :| :|:| :|  | ::|:
Db        149 ELPAAHLI-GAWMEQRLDWEASQEEAFLRSGVQFSSTDGLALPRDGIYYLYCHVGYRGRA 207

Qy         69 CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP----EGAEAXP---------- 113
               |:          |      |: : |   :    | :|    |||| :
Db        208 PPA---------GRGRARSLTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDSVGYRSL 258

Qy        114 WYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
              ||  :  ||: |: :|:|:   |: || :|:   |: :|| :
Db        259 WYTSVGFGGLVQIRSGERVYVNISHPDMVDY-RRGKTFFGAV 299


RESULT 162
Q2I7F4_ONCMY
ID   Q2I7F4_ONCMY   PRELIMINARY;   PRT;   238 AA.
AC   Q2I7F4;
DT   07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT   07-MAR-2006, sequence version 1.
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DT   07-MAR-2006, entry version 1.
DE   TNF superfamily member 14.
GN   Name=LIGHT;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Anterior kidney;
RA   Glenney G., Wiens G.D.;
RT   "Early Diversification of the Tumor Necrosis Factor Superfamily in
RT   Teleosts: Genomic Characterization and Expression Analysis.";
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ218470; ABC84585.1; -; mRNA.
SQ   SEQUENCE   238 AA;  26408 MW;  DF5C690058364EDF CRC64;

  Query Match             19.6%;  Score 154;  DB 2;  Length 238;
  Best Local Similarity   30.5%;  Pred. No. 3.5e-06;
  Matches   46;  Conservative   30;  Mismatches   57;  Indels   18;  Gaps    8;

Qy          8 PSDXPVAHVVANPQA---EGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF 64
              || :||||: | |||    :| : | | :|  :| : :| :| :||:  || | :||:: |
Db         99 PS-KPVAHLTAGPQAPHGDGVMVW-NMQAEPIL-HEMEYKDGKLVIQKEGYYYVYSKIFF 155

Qy         65 XGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGV 123
              :      |  ||:: |    |   :: || :     :|  |:  : :      |||||
Db        156 S-----EVDVAFTHSVCRTTPRYLGKDIELLKS-----RRYHPKFGKMMSTSNS-YLGGV 204

Qy        124 FQLEXGDRLSAEINRPDYLDFAESGQVYFGI 154
              | | : | :  ::     :    | :  |||
Db        205 FHLFEDDSIFVKVKNVTQVRIQHSTENVFGI 235


RESULT 163
Q5SP42_HUMAN
ID   Q5SP42_HUMAN   PRELIMINARY;   PRT;   158 AA.
AC   Q5SP42;
DT   21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   21-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Lymphotoxin alpha (TNF superfamily, member 1) (Fragment).
GN   Name=LTA; ORFNames=DAQB-87N14.7-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AL929587; CAI18647.1; -; Genomic_DNA.
DR   SMR; Q5SP42; 62-158.
DR   Ensembl; ENSG00000173503; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER     158    158
SQ   SEQUENCE   158 AA;  17200 MW;  A4C76C27B271AA95 CRC64;

  Query Match             19.5%;  Score 153;  DB 2;  Length 158;
  Best Local Similarity   33.3%;  Pred. No. 2.5e-06;
  Matches   30;  Conservative   20;  Mismatches   36;  Indels    4;  Gaps    1;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG-- 68
              :| ||:: :|  :  | |      | | :|  | :| |:||: |:| :||||:|:|:
Db         62 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS 121

Qy         69 --CPSTHVLLTHTISRIAVSYQTXVNLLSA 96
                |: : | | :   :  |  :| |||:
Db        122 PKATSSPLYLAHEVQLFSSQYPFHVPLLSS 151


RESULT 164
Q6DHG9_BRARE
ID   Q6DHG9_BRARE   PRELIMINARY;   PRT;   299 AA.
AC   Q6DHG9;
DT   16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT   16-AUG-2004, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Zgc:92320.
GN   ORFNames=zgc:92320;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole;
RA   Strausberg R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC076005; AAH76005.1; -; mRNA.
DR   ZFIN; ZDB-GENE-040718-335; zgc:92320.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
```

```
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   299 AA;  33526 MW;  BA776793D2F11ED5 CRC64;

  Query Match             19.4%;  Score 152.5;  DB 2;  Length 299;
  Best Local Similarity   28.0%;  Pred. No. 6.5e-06;
  Matches   49;  Conservative   29;  Mismatches   60;  Indels   37;  Gaps    8;

Qy          3 SSSRTPSDXPVAHVVANPQAEGQ--LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              : | ||  :     : | :  ||    | : :  | | | ||| | :|||| ||| |||
Db        133 TGSYTPESEKDGAGLPNRKVYGQKIQSWESEKGLAFLQN-VELSDGELVVPQAGLYYIYS 191

Qy         61 QVLFXG--------------------QGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXS 99
              |  |:                   :| |    :| :   ::: ||| :: |:   ::
Db        192 QTYFRHTLIEEDESAREDEYGSMGESVRGKP----MLQYVYKKVS-SYQVPILLMKNART 246

Qy        100 PC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
              |  |::  |  :      ||  |:||| :|||:   ::    :|  |    :||
Db        247 TCWSRDSEYGLYS------IYQAGLFQLGSGDRVFVTVSNVSTIDMDEKSS-FFG 294


RESULT 165
Q8MJ19_MACMU
ID   Q8MJ19_MACMU   PRELIMINARY;   PRT;   154 AA.
AC   Q8MJ19;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Fas ligand CD178 (Fragment).
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22937400; PubMed=14576776; DOI=10.1038/sj.cdd.4401289;
RA   Arnoult D., Petit F., Lelievie J.D., Lecossier D., Hance A.,
RA   Monceaux V., Ho Tsong Fang R., Huntrel B., Ameisen J.C., Estaquier J.;
RT   "Caspase-dependent and -independent T-cell death pathways in
RT   pathogenic simian immunodeficiency virus infection: relationship to
RT   disease progression.";
RL   Cell Death Differ. 10:1240-1252(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Hance A.J., Lecossier D., Estaquier J.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF530076; AAM95636.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER     154    154
SQ   SEQUENCE   154 AA;  17410 MW;  971A43779E029449 CRC64;

  Query Match             19.1%;  Score 150.5;  DB 2;  Length 154;
  Best Local Similarity   30.2%;  Pred. No. 4.2e-06;
  Matches   42;  Conservative   24;  Mismatches   54;  Indels   19;  Gaps    6;

Qy          8 PSDXP-------VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              || :|       |||:   | :    |:| :     || :||: :   ||:   ||| :|
Db         24 PSPPPEKKEQRKVAHLTGKPNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVY 82

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPI 118
              |:| |:|| |  |:: |:| :       | | :| :   ::| |          : |
Db         83 SKVYFRGQSC--TNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-------TTGQMWAHSS 133

Qy        119 YLGGVFQLEXGDRLSAEIN 137
              ||| || | : | |   ::
Db        134 YLGAVFNLTSADHLYVNVS 152


RESULT 166
TNFC_MACEU
ID   TNFC_MACEU     STANDARD;      PRT;   250 AA.
AC   Q9XT47;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1999, sequence version 1.
DT   07-FEB-2006, entry version 29.
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   Name=LTB; Synonyms=TNFC, TNFSF3;
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Mammary gland;
RX   MEDLINE=20012639; PubMed=10547148; DOI=10.1089/107999099313028;
RA   Harrison G.A., Deane E.M.;
RT   "cDNA sequence of the lymphotoxin beta chain from a marsupial,
RT   Macropus eugenii (Tammar wallaby).";
RL   J. Interferon Cytokine Res. 19:1099-1102(1999).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AF119337; AAD41774.1; -; mRNA.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    250       Lymphotoxin-beta.
FT                                /FTId=PRO_0000185487.
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FT   TOPO_DOM      1     26       Cytoplasmic (Potential).
FT   TRANSMEM     27     47       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     48    250       Extracellular (Potential).
FT   CARBOHYD    228    228       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   250 AA;  26143 MW;  AD37FB975452FE84 CRC64;

  Query Match             19.1%;  Score 150.5;  DB 1;  Length 250;
  Best Local Similarity   23.0%;  Pred. No. 8e-06;
  Matches   40;  Conservative   40;  Mismatches   73;  Indels   21;  Gaps    6;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ--LVVPSEGLYLI 58
              | | |     :| ||::   ::   |:|::    | | :| :   ::  | :| :|:| :
Db         76 VESRSDLSPIPPAAHLIGIAKSSHGLRWVSGYEEAFLKSGTQFLGDEGLLALPQDGIYFL 135

Qy         59 YSQVLFXGQ-----------GCPSTHVLLTHTISRI-AVSYQTXVNLL----SAIXSPC 101
              |  : ::|:             | |   | |:  : |    |   :  ||      :: |
Db        136 YCHIGYRGRAPSGGEQFRSQAGDPGVPVTLSSQLFRARGASGSGEPELLLQGFETVTPPV 195

Qy        102 QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
              |     | : : ||  :  ||: || :|:::   ::  : :||   |: :|| :
Db        196 QHARGVG-QGPLWYATVGFGGLVQLRGGEKIYVNVSHLELVDF-RRGKTFFGAV 247


RESULT 167
TNFL6_FELCA
ID   TNFL6_FELCA    STANDARD;      PRT;   280 AA.
AC   Q861W5;
DT   07-MAR-2006, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2003, sequence version 1.
DT   07-MAR-2006, entry version 14.
DE   Tumor necrosis factor ligand superfamily member 6 (Fas antigen ligand)
DE   (Fas ligand) (CD178 antigen) [Contains: Tumor necrosis factor ligand
DE   superfamily member 6, membrane form; Tumor necrosis factor ligand
DE   superfamily member 6, soluble form].
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=99053606; PubMed=9839871; DOI=10.1016/S0165-2427(98)00151-2;
RA   Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Tsubota K.,
RA   Mikami T., Ohno K., Watari T., Tsujimoto H., Hasegawa A.;
RT   "Molecular cloning of feline Fas antigen and Fas ligand cDNAs.";
RL   Vet. Immunol. Immunopathol. 65:161-172(1998).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC       transduces the apoptotic signal into cells. May be involved in
CC       cytotoxic T cell mediated apoptosis and in T cell development.
CC       TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC       peripheral tolerance, in the antigen-stimulated suicide of mature
CC       T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
CC       modulates its effects (By similarity).
CC   -!- SUBUNIT: Homotrimer (Probable).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AB009280; BAC76426.1; -; mRNA.
DR   HSSP; P01374; 1TNR.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    280       Tumor necrosis factor ligand superfamily
FT                                member 6, membrane form.
FT                                /FTId=PRO_0000227011.
FT   CHAIN       129    280       Tumor necrosis factor ligand superfamily
FT                                member 6, soluble form (By similarity).
FT                                /FTId=PRO_0000227012.
FT   TOPO_DOM      1     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    101       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM    102    280       Extracellular (Potential).
FT   COMPBIAS      4     69       Pro-rich.
FT   COMPBIAS     45     64       Poly-Pro.
FT   SITE        128    129       Cleavage (By similarity).
FT   CARBOHYD    183    183       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    249    249       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    259    259       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    201    232       Potential.
SQ   SEQUENCE   280 AA;  31361 MW;  6AA7E2DE1F1A6B5C CRC64;

  Query Match             19.1%;  Score 150.5;  DB 1;  Length 280;
  Best Local Similarity   28.2%;  Pred. No. 9.3e-06;
  Matches   44;  Conservative   30;  Mismatches   65;  Indels   17;  Gaps    7;

Qy          8 PSD----XPVAHVVANPQAEG-QLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 62
              ||:    : |||:   | :    |:| :    ||: :||: :   ||:   |:| :||:|
Db        136 PSEKRELRKVAHLTGKPNSRSIPLEWEDTYGIALV-SGVKYKKGGLVINDTGMYFVYSKV 194

Qy         63 LFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLG 121
              |:|| |   :  | | :       | | :| :   ::: |          : |    |||
Db        195 NFRGQSC--NNQPLNHKVYMRNSKYPQDLVLMEGKMMNYC-------TTGQMWARSSYLG 245

Qy        122 GVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              || | : | |   ::    : | || : :||:  |           .
Db        246 AVFNLTSADHLYVNVSELSLVSFEES-KTFFGLYKL 280


RESULT 168
TNFC_MOUSE
ID   TNFC_MOUSE     STANDARD;      PRT;   306 AA.
AC   P41155;
DT   01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1995, sequence version 1.
DT   07-FEB-2006, entry version 39.
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3).
GN   Name=Ltb; Synonyms=Tnfc, Tnfsf3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RX   MEDLINE=95148600; PubMed=7846035;
RA   Pokholok D.K., Maroulakou I.G., Kuprash D.V., Alimzhanov M.B.,
RA   Kozlov S.V., Novobrantseva T.I., Turetskaya R.L., Green J.E.,
RA   Nedospasov S.A.;
RT   "Cloning and expression analysis of the murine lymphotoxin beta
RT   gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:674-678(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=95088371; PubMed=7995944;
RA   Lawton P., Nelson J., Tizard R., Browning J.L.;
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RT   "Characterization of the mouse lymphotoxin-beta gene.";
RL   J. Immunol. 154:239-246(1995).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=129;
RX   PubMed=14656967; DOI=10.1101/gr.1736803;
RA   Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA   Campbell R.D., Hood L.;
RT   "Analysis of the gene-dense major histocompatibility complex class III
RT   region and its comparison to mouse.";
RL   Genome Res. 13:2621-2636(2003).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Potential).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U12029; AAA67716.1; -; Genomic_DNA.
DR   EMBL; U16984; AAB60493.1; -; Genomic_DNA.
DR   EMBL; U16985; AAA70089.1; -; mRNA.
DR   EMBL; U06950; AAA18592.1; -; Unassigned_DNA.
DR   EMBL; AF109719; AAC82483.1; -; Genomic_DNA.
DR   PIR; I49139; I49139.
DR   Ensembl; ENSMUSG00000024399; Mus musculus.
DR   MGI; MGI:104796; Ltb.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0048535; P:lymph node development; IMP.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    306       Lymphotoxin-beta.
FT                                /FTId=PRO_0000185490.
FT   TOPO_DOM      1     27       Cytoplasmic (Potential).
FT   TRANSMEM     28     48       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     49    306       Extracellular (Potential).
FT   CARBOHYD     98     98       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   306 AA;  32329 MW;  B7D276AB84A22549 CRC64;

  Query Match             19.1%;  Score 150;  DB 1;  Length 306;
  Best Local Similarity   24.7%;  Pred. No. 1.2e-05;
  Matches   40;  Conservative   32;  Mismatches   64;  Indels   26;  Gaps    5;

Qy          10 DXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ-LVVPSEGLYLIYSQVLFXGQG 68
               ::| ||::    :   | |   :  | | :| :       | :| :|:| :|  | ::|:
Db         152 ELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRT 211

Qy          69 CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETP----EGAEAXP---------- 113
                 |:          |      |: : |   :    | :|    |||| :
Db         212 PPA---------GRSRARSLTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSL 262

Qy         114 WYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
               ||  :  ||: || :|:|:   |: || :|:   |: :|| :
Db         263 WYTSVGFGGLAQLRSGERVYVNISHPDMVDY-RRGKTFFGAV 303
```

```
RESULT 169
Q3T4H6_MACEU
ID   Q3T4H6_MACEU   PRELIMINARY;   PRT;   250 AA.
AC   Q3T4H6;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Lymphotoxin beta.
GN   Name=LTB;
OS   Macropus eugenii (Tammar wallaby).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=16103651; DOI=10.1159/000086379;
RA   Cross J.G., Harrison G.A., Coggill P., Sims S., Beck S., Deakin J.E.,
RA   Graves J.A.;
RT   "Analysis of the genomic region containing the tammar wallaby
RT   (Macropus eugenii) orthologues of MHC class III genes.";
RL   Cytogenet. Genome Res. 111:110-117(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Harrison G.G., Cross J.G., Deakin J.E., Marshall Graves J.A.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY853666; AAZ99792.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   250 AA;  26083 MW;  5D65EBB7084D1ED7 CRC64;

  Query Match             18.9%;  Score 148.5;  DB 2;  Length 250;
  Best Local Similarity   23.0%;  Pred. No. 1.2e-05;
  Matches   40;  Conservative   40;  Mismatches   73;  Indels   21;  Gaps    6;

Qy           1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQ--LVVPSEGLYLI 58
               | | |     :| ||::   ::   |:|::    | | :| :   ::   | :| :|:| :
Db          76 VESRSDLSPIPPAAHLIGIAKSSHGLRWVSGYEEAFLKSGTQFLGDEGLLALPQDGIYSL 135

Qy          59 YSQVLFXGQ-----------GCPSTHVLLTHTISRI-AVSYQTXVNLL----SAIXSPC 101
               |  : ::|:           | |   | |:  : |    |   :  ||      :: |
Db         136 YCHIGYRGRAPSGGEQFRSQAGDPGVPVTLSSQLFRARGASGSGEPELLLQGFETVTPPV 195

Qy         102 QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGII 155
               |     | : : ||  :  ||: || :|:::   ::  : :||   |: :|| :
Db         196 QHARGVG-QGPLWYATVGFGGLVQLRGGEKIYVNVSHLELVDF-RRGKTFFGAV 247


RESULT 170
TNFC_PIG
ID   TNFC_PIG       STANDARD;      PRT;   150 AA.
AC   Q9TSV8;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 26.
DE   Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
DE   necrosis factor ligand superfamily member 3) (Fragment).
GN   Name=LTB; Synonyms=TNFC, TNFSF3;
```

```
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Large white; TISSUE=Fibroblast;
RX   MEDLINE=21108615; PubMed=11169259;
RX   DOI=10.1034/j.1399-0039.2001.057001055.x;
RA   Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
RA   Renard C.;
RT   "Sequence of the swine major histocompatibility complex region
RT   containing all non-classical class I genes.";
RL   Tissue Antigens 57:55-65(2001).
CC   -!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
CC       role in immune response regulation. Provides the membrane anchor
CC       for the attachment of the heterotrimeric complex to the cell
CC       surface.
CC   -!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
CC       (less prevalent) two LTA and one LTB subunits.
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251914; CAB63851.1; -; Genomic_DNA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein.
FT   CHAIN        <1    150       Lymphotoxin-beta.
FT                                 /FTId=PRO_0000185492.
FT   CARBOHYD     128   128       N-linked (GlcNAc. . .) (Potential).
FT   NON_TER        1     1
SQ   SEQUENCE   150 AA;  16423 MW;  FE5C4CC657658B48 CRC64;

  Query Match             18.6%;  Score 146.5;  DB 1;  Length 150;
  Best Local Similarity   24.8%;  Pred. No. 9.8e-06;
  Matches   37;  Conservative   35;  Mismatches   54;  Indels   23;  Gaps    6;

Qy         24 GQ-LQWLNRRANALLANGVELRDNQ-LVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTIS 81
              || | |  ::  | | :| :    : | :| :||| :|  | ::|:  |      |  :::
Db          5 GQGLGWEAKKEEAFLRSGTQFSGAEGLALPQDGLYYLYCHVGYRGRAPPPGGDPLDRSVT 64

Qy         82 RIAVSYQT-------------XVNLLSAIXSPCQRETPEGAEAXP-WYEPIYLGGVFQL 126
                ::  |:                :   :: :: | :|      | :| ||  :  ||: ||
Db         65 LLSRLYRAGGAYGPGTPELLLEGAETVTPVLDPSRRH-----EYGPLWYTSVGFGGLVQL 119

Qy        127 EXGDRLSAEINRPDYLDFAESGQVYFGII 155
                :|:|:   |: || :|:   |: :|| :
Db        120 RRGERVYVNISHPDMVDY-RRGKTFFGAV 147


RESULT 171
Q6J3Q6_CANFA
ID   Q6J3Q6_CANFA   PRELIMINARY;   PRT;   131 AA.
AC   Q6J3Q6;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Fas ligand (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Spee B., Arends B., Favier R., Penning L.C., Rothuizen J.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY603042; AAT37155.1; -; mRNA.
DR   HSSP; P01375; 1A8M.
DR   Ensembl; ENSCAFG00000014678; Canis familiaris.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002961; TNF_C.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01237; TNFC.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   131 AA;  14953 MW;  29368EC38D2D8909 CRC64;

  Query Match             18.2%;  Score 143;  DB 2;  Length 131;
  Best Local Similarity   29.3%;  Pred. No. 1.8e-05;
  Matches   39;  Conservative   25;  Mismatches   57;  Indels   12;  Gaps    5;

Qy         26 LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIAV 85
              |:|  :    ||: :||: :   ||:   ||| :||:| |:|| |   :  | | :
Db         10 LEWEDTYGIALV-SGVKYKKGGLVINDTGLYFVYSKVYFRGQSC--NNKPLNHKVYMRNS 66

Qy         86 SYQTXVNLLSA-IXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDF 144
                |  :: |:   |:: |           : |    ||| || | : | |   ::    : |
Db         67 KYPQDLMLMEGKIMNYC-------TTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVSF 119

Qy        145 AESGQVYFGIIAL 157
                || : :||:  |
Db        120 EES-KTFFGLYKL 131


RESULT 172
Q9DDZ5_BRARE
ID   Q9DDZ5_BRARE   PRELIMINARY;   PRT;   214 AA.
AC   Q9DDZ5;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   TRAIL-like protein.
GN   Name=tnfsf10l;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Bobe J., Goetz F.W.;
```

```
RT   "Molecular cloning and expression of a TNF receptor and two TNF
RT   ligands in the fish ovary.";
RL   Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF250041; AAG47640.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSDARG00000004196; Danio rerio.
DR   ZFIN; ZDB-GENE-010801-1; tnfsf10l.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   214 AA;  24093 MW;  98C002474FF691AA CRC64;

  Query Match             18.1%;  Score 142;  DB 2;  Length 214;
  Best Local Similarity   26.8%;  Pred. No. 4.3e-05;
  Matches   48;  Conservative   29;  Mismatches   64;  Indels   38;  Gaps    9;

Qy          7 TPSDXPVAHVV-------ANPQAE-GQLQ-------------WLNRRANALLANGVELRD 45
              |   :| ||:         : ||::  | |              | |:   | | | : | :
Db         44 TVMQRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLYN-MTLTN 102

Qy         46 NQLVVPSEGLYLIYSQVLFXGQGCPS-------THVLLTHTISRIAVSYQTXVNLLSAIX 98
              :| || :| | :|||| |:    ||        :| |:      :   ||  :: ||  ::
Db        103 GRLRVPQDGRYYLYSQVYFR-YPSPSDSDQSSVSHQLVQCIYKK--TSYLNPIQLLKGVG 159

Qy         99 SPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              : |     | |         :| ||:|:| :|| :   :: |  : : |    |||   |
Db        160 TKCWAPDAEYA-----LHSVYQGGLFELRAGDEVFVSVSSPTMV-YGEDSSSYFGAFRL 212


RESULT 173
Q90WT9_CHICK
ID   Q90WT9_CHICK   PRELIMINARY;   PRT;   287 AA.
AC   Q90WT9;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 18.
DE   TNF-related apoptosis inducing ligand-like protein.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Bridgham J.T., Johnson A.L.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY057941; AAL23702.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSGALG00000007240; Gallus gallus.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   287 AA;  32092 MW;  DB06E1C95087B108 CRC64;

  Query Match             18.1%;  Score 142;  DB 2;  Length 287;
  Best Local Similarity   25.4%;  Pred. No. 6.3e-05;
  Matches   43;  Conservative   32;  Mismatches   64;  Indels   30;  Gaps    6;

Qy         11 XPVAHVVANPQAEGQ-----------------LQWLNRRANALLANGVELRDNQLVVPS 52
              :| ||::  ||   |                 :| :   :: | | :  || :| |
Db        125 KPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRWEDSTIHSHLQN-ITYRDGRLRVNQ 183

Qy         53 EGLYLIYSQVLF----XGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEG 108
              | | :|||: |    :| |   :   |   |:    ||  :: ||  ::: |
Db        184 AGKYYVYSQIYFRYSRDGAGARVSVPQLVQCIN-WKTSYSQPILLLKGVGTKCW-----A 237

Qy        109 AEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||:     :| ||:|:|::|| |    ::    :|::::  |||   |
Db        238 PEAEYGLHALYQGGLFELKAGDELFVSVSSL-AIDYSDAAASYFGAFRL 285


RESULT 174
Q7ZYX9_BRARE
ID   Q7ZYX9_BRARE   PRELIMINARY;   PRT;   317 AA.
AC   Q7ZYX9;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Tnfsf10l protein.
GN   Name=tnfsf10l;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB; TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB; TISSUE=Whole body;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC044336; AAH44336.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSDARG00000004196; Danio rerio.
DR   ZFIN; ZDB-GENE-010801-1; tnfsf10l.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
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DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   317 AA;  35465 MW;  68F76BC1A40DCE9F CRC64;

  Query Match             18.1%;  Score 142;  DB 2;  Length 317;
  Best Local Similarity   26.8%;  Pred. No. 7.2e-05;
  Matches   48;  Conservative   29;  Mismatches   64;  Indels   38;  Gaps    9;

Qy          7 TPSDXPVAHVV-------ANPQAE-GQLQ------------WLNRRANALLANGVELRD 45
              |   :| ||:        : ||::  | |             | |:   | | | : | :
Db        147 TVMQRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLYN-MTLTN 205

Qy         46 NQLVVPSEGLYLIYSQVLFXGQGCPS-------THVLLTHTISRIAVSYQTXVNLLSAIX 98
               :| || :| | :|||| |:    ||        :| |:     :   ||  :: ||  ::
Db        206 GRLRVPQDGRYYLYSQVYFR-YPSPSDSDQSSVSHQLVQCIYKK--TSYLNPIQLLKGVG 262

Qy         99 SPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              : |      | |         :| ||:|:| :|| :   :: |  : : |    |||   |
Db        263 TKCWAPDAEYA-----LHSVYQGGLFELRAGDEVFVSVSSPTMV-YGEDSSSYFGAFRL 315


RESULT 175
Q50D53_GASAC
ID   Q50D53_GASAC   PRELIMINARY;   PRT;   234 AA.
AC   Q50D53;
DT   07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT   07-JUN-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Tumor necrosis factor ligand superfamily member 13B.
OS   Gasterosteus aculeatus (Three-spined stickleback).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC   Gasterosteidae; Gasterosteus.
OX   NCBI_TaxID=69293;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15790847; DOI=10.1126/science.1107239;
RA   Colosimo P.F., Hosemann K.E., Balabhadra S., Villarreal G. Jr,
RA   Dickson M., Grimwood J., Schmutz J., Myers R.M., Schluter D.,
RA   Kingsley D.M.;
RT   "Widespread parallel evolution in sticklebacks by repeated fixation of
RT   Ectodysplasin alleles.";
RL   Science 307:1928-1933(2005).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY897589; AAY27077.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   234 AA;  26160 MW;  A58662BC46760A35 CRC64;

  Query Match             17.9%;  Score 140.5;  DB 2;  Length 234;
  Best Local Similarity   26.4%;  Pred. No. 6.7e-05;
  Matches   42;  Conservative   33;  Mismatches   69;  Indels   15;  Gaps    5;

Qy          2 RSSSRTPSD--XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIY 59
              : | | |:   :  |:    |  :| :  :    :|   | :  ::|::||  :| ||::
Db         87 QGSCRAPTSFLQLTANTNKQPDIKGNITVIPWTVSAQQGNAISQKENRIVVQEDGYYLVF 146

Qy         60 SQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIY 119
```

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                ||||:       |:: : : :|   : :|:  ||      | :| |:   |:      |
Db        147 GQVLFKSPSKVMGHIIQSLSSTR---TERTPTELLC-----CLQEMPDKTPAN----TCY 194

Qy        120 LGGVFQLEXGDRLSAEI-NRPDYLDFAESGQVYFGIIAL 157
              || || : | |   |  ||  |   ::   :||:| |
Db        195 TAGVVQLLQDDELELVIPYRPHSLISMDADSTFFGVIQL 233


RESULT 176
Q9WV90_MARMO
ID   Q9WV90_MARMO   PRELIMINARY;   PRT;   169 AA.
AC   Q9WV90;
DT   01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1999, sequence version 1.
DT   07-FEB-2006, entry version 24.
DE   Fas ligand (Fragment).
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Sciuridae; Xerinae; Marmotini; Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Healthy liver;
RX   MEDLINE=20010026; PubMed=10540161;
RX   DOI=10.1046/j.1365-2249.1999.01010.x;
RA   Hodgson P.D., Grant M.D., Michalak T.I.;
RT   "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT   chronic woodchuck viral hepatitis.";
RL   Clin. Exp. Immunol. 118:63-70(1999).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF152368; AAD38387.1; -; mRNA.
DR   HSSP; P50591; 1DG6.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008064; Fas_ligand.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR15161; Fas_ligand; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01681; FASLIGAND.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER      1      1
FT   NON_TER    169    169
SQ   SEQUENCE   169 AA;  19274 MW;  FDE395B014717B6B CRC64;

  Query Match             17.8%;  Score 140;  DB 2;  Length 169;
  Best Local Similarity   26.5%;  Pred. No. 4.9e-05;
  Matches   39;  Conservative   30;  Mismatches   62;  Indels   16;  Gaps    6;

Qy          7 TPSDXP----VAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ 61
              :|||:       ||:   | :     |:| :    :|: :||: :   ||:   ||| :||:
Db         33 SPSDKKALRRAAHLTGKPNSRSSPLEWEDTYGISLI-SGVKYQKGGLVINDTGLYFVYSK 91

Qy         62 VLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              : |:|| |   :  |:| :       | | :| :   ::: |     :  |     || .
Db         92 IYFRGQSC--NNQPLSHKVYVKNSKYPQDLVLMEGKMMNYC-------TTGQMWARSSYL 142

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAES 147
              | ||   : | |   ::    ::| ||
Db        143 GAVFNFTSNDHLYVNVSELSLINFEES 169
```

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RESULT 177
CD40L_RAT
ID   CD40L_RAT      STANDARD;      PRT;   260 AA.
AC   Q9Z2V2; Q9R254;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   06-JUN-2002, sequence version 2.
DT   07-MAR-2006, entry version 37.
DE   CD40 ligand (CD40-L) (Tumor necrosis factor ligand superfamily member
DE   5) (CD154 antigen) [Contains: CD40 ligand, membrane form; CD40 ligand,
DE   soluble form].
GN   Name=Cd40lg; Synonyms=Cd40l, Tnfsf5;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Sprague-Dawley; TISSUE=Splenocyte;
RX   MEDLINE=20284949; PubMed=10826698;
RA   Hallett K.M., Oaks M.K.;
RT   "Nucleotide sequence of the rat CD40 ligand.";
RL   DNA Seq. 10:405-406(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=PVG; TISSUE=Spleen;
RA   Daniel K.C., Foss Y., Moussavi A., Macary P., Kemeny D.M.,
RA   Farzaneh F., Gaken J.A.;
RT   "Cloning and sequencing of rat CD40 ligand.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC       proliferation in the absence of co-stimulus as well as IgE
CC       production in the presence of IL-4. Involved in immunoglobulin
CC       class switching (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF116582; AAD22460.1; -; mRNA.
DR   EMBL; AF013985; AAD09323.1; -; mRNA.
DR   HSSP; P29965; 1ALY.
DR   SMR; Q9Z2V2; 115-260.
DR   Ensembl; ENSRNOG00000000871; Rattus norvegicus.
DR   RGD; 708418; Tnfsf5.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0005174; F:CD40 receptor binding; ISS.
DR   GO; GO:0042100; P:B cell proliferation; ISS.
DR   GO; GO:0006954; P:inflammatory response; ISS.
DR   GO; GO:0007159; P:leukocyte adhesion; ISS.
DR   GO; GO:0030168; P:platelet activation; ISS.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR13978:SF4; TNF_5; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01702; CD40LIGAND.
DR   ProDom; PD008600; TNF_5; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    260       CD40 ligand, membrane form.
FT                                /FTId=PRO_0000034494.
FT   CHAIN       112    260       CD40 ligand, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034495.
FT   TOPO_DOM      1     22       Cytoplasmic (Potential).
FT   TRANSMEM     23     43       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     44    260       Extracellular (Potential).
FT   SITE        111    112       Cleavage (By similarity).
FT   CARBOHYD    239    239       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    177    217       Potential.
FT   CONFLICT     41     41       P -> L (in Ref. 1).
FT   CONFLICT    114    114       R -> K (in Ref. 1).
FT   CONFLICT    255    255       I -> F (in Ref. 1).
SQ   SEQUENCE   260 AA;  29260 MW;  B3D3757DE60DB73A CRC64;

  Query Match             17.2%;  Score 135;  DB 1;  Length 260;
  Best Local Similarity   27.0%;  Pred. No. 0.00026;
  Matches   47;  Conservative   26;  Mismatches   39;  Indels   62;  Gaps    8;

Qy          6 RTPSDXPV-AHVV--ANPQAEGQLQWLNRRANALLANGVELRD-NQLVVPSEGLYLIYSQ 61
              |   |: : ||||  ||  |   |||  :    : :| | | :  || |  |||| :|:|
Db        114 RGDEDPQIAAHVVSEANSNAASVLQWAKKGYYTMKSNLVVLENGRQLTVKREGLYYVYTQ 173

Qy         62 VLFXGQGCP----------------STHVLL----THTISRIAVSYQTXVNLLSAIXSP 100
              | |:    |                |  :||    ||: |::
Db        174 VTFCSNREPLSQRPFIVSLWLKPSSGSERILLRAANTHSSSKL---------------- 216

Qy        101 CQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGI 154
              |::::            |:|||||:|::|  :        :::  |: ||  ||
Db        217 CEQQS-----------IHLGGVFELQAGASV--------FVNVTEASQVIHGI 250


RESULT 178
Q8K3G0_RAT
ID   Q8K3G0_RAT     PRELIMINARY;   PRT;   287 AA.
AC   Q8K3G0;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   TNF-related apoptosis inducing ligand.
GN   Name=Tnfsf10;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DA;
RA   Mueller A.M., Giegerich G.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AY115578; AAM49797.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   SMR; Q8K3G0; 123-287.
DR   Ensembl; ENSRNOG00000013269; Rattus norvegicus.
DR   RGD; 628734; Tnfsf10.
DR   GO; GO:0006917; P:induction of apoptosis; NAS.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   287 AA;  32980 MW;  CA4F5B5D7C833FEC CRC64;

  Query Match             16.9%;  Score 132.5;  DB 2;  Length 287;
  Best Local Similarity   26.5%;  Pred. No. 0.00052;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   17;  Gaps    4;

Qy         28 WLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIA--- 84
              | : |      | | ||: :||:  |||| ||||  :: :        ::    ||
```

```
Db        158 WESSRRGHSFLNHVHLRNGELVIQEEGLYYIYSQTYYRFKEAKEASKTVSKDGGRIKQMV 217

Qy         85 ------VSYQTXVNLLSAIXSPC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEIN 137
                  ||  :: |: : :: |  ||   |  :      || ||:|:|:: ||:   :
Db        218 QYIYKYTSYPDPILLMKSARNSCWSREAEYGLYS------IYQGGLFELKENDRIFVSVT 271

Qy        138 RPDYLDFAESGQVYFG 153
                :|      :||
Db        272 NEHLMDLDHEAS-FFG 286


RESULT 179
CD40L_MOUSE
ID   CD40L_MOUSE    STANDARD;      PRT;   260 AA.
AC   P27548;
DT   01-AUG-1992, integrated into UniProtKB/Swiss-Prot.
DT   14-AUG-2001, sequence version 2.
DT   07-MAR-2006, entry version 57.
DE   CD40 ligand (CD40-L) (Tumor necrosis factor ligand superfamily member
DE   5) (CD154 antigen) (TNF-related activation protein) (TRAP) (T cell
DE   antigen Gp39) [Contains: CD40 ligand, membrane form; CD40 ligand,
DE   soluble form].
GN   Name=Cd40lg; Synonyms=Cd40l, Tnfsf5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92244364; PubMed=1374165; DOI=10.1038/357080a0;
RA   Armitage R., Fanslow W., Sato T.A., Clifford K.N., Strockbine L.,
RA   Macduff B.M., Anderson D.M., Gimpel S.D., Davis-Smith T.,
RA   Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D.,
RA   Spriggs M.K.;
RT   "Molecular and biological characterization of a murine ligand for
RT   CD40.";
RL   Nature 357:80-82(1992).
RN   [2]
RP   SEQUENCE REVISION TO 198.
RA   Spriggs M.K.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 1-52 AND 137-260.
RC   STRAIN=129/Sv; TISSUE=Liver;
RX   MEDLINE=94344153; PubMed=7520529; DOI=10.1016/0161-5890(94)90009-4;
RA   Tsitsikov E.N., Ramesh N., Geha R.S.;
RT   "Structure of the murine CD40 ligand gene.";
RL   Mol. Immunol. 31:895-900(1994).
RN   [4]
RP   SIMILARITY TO THE TNF FAMILY.
RX   MEDLINE=92310561; PubMed=1377364; DOI=10.1038/358026b0;
RA   Farrah T., Smith C.A.;
RT   "Emerging cytokine family.";
RL   Nature 358:26-26(1992).
RN   [5]
RP   3D-STRUCTURE MODELING OF 115-260.
RX   MEDLINE=93200072; PubMed=8095800;
RA   Peitsch M.C., Jongeneel C.V.;
RT   "A 3-D model for the CD40 ligand predicts that it is a compact trimer
RT   similar to the tumor necrosis factors.";
RL   Int. Immunol. 5:233-238(1993).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC       proliferation in the absence of co-stimulus as well as IgE
CC       production in the presence of IL-4. Involved in immunoglobulin
CC       class switching (By similarity).
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form.
CC   -!- TISSUE SPECIFICITY: Specifically expressed on activated CD4+ T-
CC       lymphocytes.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X65453; CAA46448.2; -; mRNA.
DR   EMBL; S71858; AAC13639.1; -; Genomic_DNA.
DR   EMBL; S71861; AAC13640.1; -; Genomic_DNA.
DR   PIR; S21738; S21738.
DR   PDB; 1CDA; Model; A/B/C=115-260.
DR   Ensembl; ENSMUSG00000031132; Mus musculus.
DR   MGI; MGI:88337; Cd40lg.
DR   GO; GO:0005887; C:integral to plasma membrane; ISS.
DR   GO; GO:0005625; C:soluble fraction; ISS.
DR   GO; GO:0005174; F:CD40 receptor binding; ISS.
DR   GO; GO:0006916; P:anti-apoptosis; ISS.
DR   GO; GO:0042100; P:B cell proliferation; ISS.
DR   GO; GO:0006954; P:inflammatory response; ISS.
DR   GO; GO:0045190; P:isotype switching; IDA.
DR   GO; GO:0007159; P:leukocyte adhesion; ISS.
DR   GO; GO:0030168; P:platelet activation; ISS.
DR   GO; GO:0051023; P:regulation of immunoglobulin secretion; IDA.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR13978:SF4; TNF_5; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01702; CD40LIGAND.
DR   ProDom; PD008600; TNF_5; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   3D-structure; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    260       CD40 ligand, membrane form.
FT                                /FTId=PRO_0000034490.
FT   CHAIN       112    260       CD40 ligand, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034491.
FT   TOPO_DOM      1     22       Cytoplasmic (Potential).
FT   TRANSMEM     23     46       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     47    260       Extracellular (Potential).
FT   SITE        111    112       Cleavage (By similarity).
FT   CARBOHYD    239    239       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    177    217
FT   CONFLICT    198    198       S -> I (in Ref. 3; AAC13640).
FT   STRAND      118    120
FT   STRAND      122    127
FT   TURN        130    132
FT   STRAND      133    133
FT   TURN        134    135
FT   STRAND      139    140
FT   STRAND      143    143
FT   TURN        144    145
FT   STRAND      148    148
FT   TURN        150    151
FT   STRAND      154    155
FT   TURN        156    158
FT   STRAND      159    161
FT   STRAND      164    164
FT   STRAND      166    176
FT   STRAND      179    180
FT   STRAND      183    184
FT   STRAND      188    195
FT   STRAND      197    198
FT   STRAND      200    200
FT   STRAND      202    209
FT   STRAND      213    214
FT   STRAND      216    217
FT   STRAND      220    230
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FT   TURN        232    233
FT   STRAND      235    242
FT   TURN        243    244
FT   STRAND      248    248
FT   STRAND      250    250
FT   TURN        251    252
FT   STRAND      253    260
SQ   SEQUENCE   260 AA;  29370 MW;  7E1AC117473672AD CRC64;

  Query Match             16.7%;  Score 131.5;  DB 1;  Length 260;
  Best Local Similarity   25.5%;  Pred. No. 0.00057;
  Matches   47;  Conservative   30;  Mismatches   38;  Indels   69;  Gaps    9;

Qy          6 RTPSDXPV-AHVV--ANPQAEGQLQWLNRRANALLANGVELRD-NQLVVPSEGLYLIYSQ 61
              |   |: : ||||  ||  |   |||  :    : :| | | :  || |  |||| :|:|
Db        114 RGDEDPQIAAHVVSEANSNAASVLQWAKKGYYTMKSNLVMLENGKQLTVKREGLYYVYTQ 173

Qy         62 VLFXGQGCPST----------------HVLL----THTISRIAVSYQTXVNLLSAIXSP 100
              | |:    ||:                   :||    ||: |::
Db        174 VTFCSNREPSSQRPFIVGLWLKPSSGSERILLKAANTHSSSQL---------------- 216

Qy        101 CQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVY-------FG 153
              |::::            ::|||||:|::|  :        :::  |: ||        ||
Db    .   217 CEQQS-----------VHLGGVFELQAGASV--------FVNVTEASQVIHRVGFSSFG 256

Qy        154 IIAL 157
              :: |
Db        257 LLKL 260


RESULT 180
Q5EAP6_BRARE
ID   Q5EAP6_BRARE   PRELIMINARY;   PRT;   219 AA.
AC   Q5EAP6;
DT   15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT   15-MAR-2005, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Zgc:113297.
GN   ORFNames=zgc:113297;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Singapore local strain; TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Singapore local strain; TISSUE=Embryo;
RG   NIH MGC Project;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; BC090312; AAH90312.1; -; mRNA.
DR   ZFIN; ZDB-GENE-050227-6; zgc:113297.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   219 AA;  24915 MW;  CDB916C8FF1A2B16 CRC64;

  Query Match             16.6%;  Score 130.5;  DB 2;  Length 219;
  Best Local Similarity   25.9%;  Pred. No. 0.00057;
  Matches   41;  Conservative   29;  Mismatches   65;  Indels   23;  Gaps    6;

Qy         11 XPVAHVVANPQ-------------AEGQLQWLNRRANALLANGVELR-DNQLVVPSEGL 55
              :|  || | :              |  :: | |     :    : |  | ::|||  |:
Db         65 KPAVHVGAKQELKQYQSLQINDEVPALDRIHWDNMNGQFIQEGLMRLSPDGEIVVPLNGI 124

Qy         56 YLIYSQVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWY 115
              | ::||| |: |   : |   |  : :   ||  :| |  | ::||      | : :  :
Db        125 YFVFSQVNFETQLGQNVH--FTQYLYKRTASYPRPVMLSKAAVTPCS-SVRSGVQLYTNH 181

Qy        116 EPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
              :    | :|:|::|||||  :    : | :   |||
Db        182 Q----GALFRLQKGDRLSLYVLDTRAVRPPQEA-TYFG 214


RESULT 181
TNF10_MOUSE
ID   TNF10_MOUSE    STANDARD;      PRT;   291 AA.
AC   P50592;
DT   01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-1996, sequence version 1.
DT   07-FEB-2006, entry version 43.
DE   Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE   apoptosis-inducing ligand) (TRAIL protein) (CD253 antigen).
GN   Name=Tnfsf10; Synonyms=Trail;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=96111955; PubMed=8777713; DOI=10.1016/1074-7613(95)90057-8;
RA   Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA   Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA   Goodwin R.G.;
RT   "Identification and characterization of a new member of the TNF family
RT   that induces apoptosis.";
RL   Immunity 3:673-682(1995).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
CC       TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
CC       possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
CC       may be modulated by binding to the decoy receptors
CC       TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
CC       induce apoptosis.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type II membrane
CC       protein (Potential).
CC   -!- TISSUE SPECIFICITY: Widespread.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
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DR   EMBL; U37522; AAC52345.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   SMR; P50592; 123-290.
DR   Ensembl; ENSMUSG00000039304; Mus musculus.
DR   MGI; MGI:107414; Tnfsf10.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Apoptosis; Cytokine; Glycoprotein; Membrane; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    291       Tumor necrosis factor ligand superfamily
FT                                member 10.
FT                                /FTId=PRO_0000185504.
FT   TOPO_DOM      1     17       Cytoplasmic (Potential).
FT   TRANSMEM     18     38       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     39    291       Extracellular (Potential).
FT   CARBOHYD     52     52       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   291 AA;  33477 MW;  3FEACAB9F0D7D802 CRC64;

  Query Match             16.3%;  Score 128.5;  DB 1;  Length 291;
  Best Local Similarity   25.7%;  Pred. No. 0.0013;
  Matches   35;  Conservative   25;  Mismatches   59;  Indels   17;  Gaps    4;

Qy         28 WLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTHTISRIA--- 84
              | : |       | |   |: :||:  |||| ||||  |: |        :::     |
Db        158 WESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQLV 217

Qy         85 ------VSYQTXVNLLSAIXSPC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEIN 137
                   ||  :: |: : :: |  |:   |  :      || ||:|:|:: ||:   :
Db        218 QYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYS------IYQGGLFELKKNDRIFVSVT 271

Qy        138 RPDYLDFAESGQVYFG 153
                :|  :    :||
Db        272 NEHLMDLDQEAS-FFG 286


RESULT 182
Q3TZR6_MOUSE
ID   Q3TZR6_MOUSE   PRELIMINARY;   PRT;   291 AA.
AC   Q3TZR6;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Activated spleen cDNA, RIKEN full-length enriched library,
DE   clone:F830228J05 product:tumor necrosis factor (ligand) superfamily,
DE   member 10, full insert sequence.
GN   Name=Tnfsf10;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Pagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
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RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK157633; BAE34141.1; -; mRNA.
DR   MGI; MGI:107414; Tnfsf10.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   291 AA;  33449 MW;  6E40EABBEED938E9 CRC64;

  Query Match             16.3%;  Score 128.5;  DB 2;  Length 291;
  Best Local Similarity   25.7%;  Pred. No. 0.0013;
  Matches   35;  Conservative   25;  Mismatches   59;  Indels   17;  Gaps    4;

Qy         28 WLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIA--- 84
              | : |     | |  |: :||:  |||| ||||  |: |       :::    |
Db        158 WESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAKDASKMVSKDKVRTKQLV 217

Qy         85 ------VSYQTXVNLLSAIXSPC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEIN 137
                    ||  :: |: : :: |  |:   |  :      || ||:|:|:: ||:   :
Db        218 QYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYS------IYQGGLFELKKNDRIFVSVT 271

Qy        138 RPDYLDFAESGQVYFG 153
                :|  :   :||
Db        272 NEHLMDLDQEAS-FFG 286


RESULT 183
Q3U5H0_MOUSE
ID   Q3U5H0_MOUSE   PRELIMINARY;   PRT;   291 AA.
AC   Q3U5H0;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A630004M21 product:tumor necrosis factor (ligand) superfamily,
DE   member 10, full insert sequence.
GN   Name=Tnfsf10;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
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RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11076159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AK153581; BAE32108.1; -; mRNA.
DR   MGI; MGI:107414; Tnfsf10.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   291 AA;  33477 MW;  3FEACAB9F0D7D802 CRC64;

  Query Match            16.3%;  Score 128.5;  DB 2;  Length 291;
  Best Local Similarity  25.7%;  Pred. No. 0.0013;
  Matches   35;  Conservative   25;  Mismatches   59;  Indels   17;  Gaps    4;

Qy         28 WLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIA--- 84
              | : |       | |  |: :||:  |||| ||||  |: |       :::    |
Db        158 WESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAEDASKMVSKDKVRTKQLV 217

Qy         85 ------VSYQTXVNLLSAIXSPC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEIN 137
                    ||  :: |: : :: |  |:   |  :      || ||:|:|:: ||:   :
Db        218 QYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYS------IYQGGLFELKKNDRIFVSVT 271

Qy        138 RPDYLDFAESGQVYFG 153
                :|  :    :||
Db        272 NEHLMDLDQEAS-FFG 286
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RESULT 184
Q5XKN3_MOUSE
ID   Q5XKN3_MOUSE   PRELIMINARY;   PRT;   303 AA.
AC   Q5XKN3;
DT   23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Hypothetical protein (Fragment).
GN   Name=Tnfsf10;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung.
RC   MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung.
RC   MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
RA   Director MGC Project;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC011469; AAH11469.1; -; mRNA.
DR   SMR; Q5XKN3; 135-302.
DR   Ensembl; ENSMUSG00000039304; Mus musculus.
DR   MGI; MGI:107414; Tnfsf10.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   303 AA;  34818 MW;  9BA648EB3CA569BE CRC64;

  Query Match             16.3%;  Score 128.5;  DB 2;  Length 303;
  Best Local Similarity   25.7%;  Pred. No. 0.0014;
  Matches   35;  Conservative   25;  Mismatches   59;  Indels   17;  Gaps    4;

Qy         28 WLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCPSTHVLLTHTISRIA--- 84
               | : |      | |  |: :||:  |||| ||||  |: |       :::    |
Db        170 WESSRKGHSFLNHVLFRNGELVIEQEGLYYIYSQTYFRFQEAKDASKMVSKDKVRTKQLV 229

Qy         85 ------VSYQTXVNLLSAIXSPC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEIN 137
                    ||  :: |: : :: |  |:   |  :      || ||:|:|:: ||:   :
Db        230 QYIYKYTSYPDPIVLMKSARNSCWSRDAEYGLYS------IYQGGLFELKKNDRIFVSVT 283

Qy        138 RPDYLDFAESGQVYFG 153
                :|  :    :||
Db        284 NEHLMDLDQEAS-FFG 298


RESULT 185
TNF11_RAT
ID   TNF11_RAT      STANDARD;      PRT;   318 AA.
AC   Q9ESE2; Q91ZI9;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 32.
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) (CD254 antigen) [Contains: Tumor
DE   necrosis factor ligand superfamily member 11, membrane form; Tumor
DE   necrosis factor ligand superfamily member 11, soluble form].
GN   Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Tibial bone;
RX   MEDLINE=20540945; PubMed=11092398;
RA   Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA   Zheng M.H.;
RT   "Cloning, sequence and functional characterization of the rat
RT   homologue of receptor activator of NF-kB ligand.";
RL   J. Bone Miner. Res. 15:2178-2186(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 266-318.
RC   STRAIN=Fischer 344;
RX   MEDLINE=21662371; PubMed=11804028;
RA   Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,
RA   Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
RA   Marks S.C. Jr.;
RT   "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT   the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";
RL   Int. J. Dev. Biol. 45:853-859(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC       TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC       Augments the ability of dendritic cells to stimulate naive T-cell
CC       proliferation. May be an important regulator of interactions
CC       between T cells and dendritic cells and may play a role in the
CC       regulation of the T cell-dependent immune response. May also play
CC       an important role in enhanced bone-resorption in humoral
CC       hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC       similarity).
CC   -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF187319; AAG17031.1; -; mRNA.
DR   EMBL; AF425669; AAL23963.1; -; mRNA.
DR   HSSP; O35235; 1JTZ.
DR   SMR; Q9ESE2; 163-318.
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DR   Ensembl; ENSRNOG00000009559; Rattus norvegicus.
DR   RGD; 620784; Tnfsf11.
DR   GO; GO:0045780; P:positive regulation of bone resorption; IMP.
DR   GO; GO:0045672; P:positive regulation of osteoclast different. . .; IMP.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Developmental protein; Differentiation; Glycoprotein;
KW   Membrane; Receptor; Signal-anchor; Transmembrane.
FT   CHAIN         1    318       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT                                /FTId=PRO_0000034518.
FT   CHAIN       141    318       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form.
FT                                /FTId=PRO_0000034519.
FT   TOPO_DOM      1     47       Cytoplasmic (Potential).
FT   TRANSMEM     48     68       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     69    318       Extracellular (Potential).
FT   SITE        140    141       Cleavage (By similarity).
FT   CARBOHYD    199    199       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    264    264       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    317    317       I -> M (in Ref. 2).
SQ   SEQUENCE   318 AA;  35370 MW;  4B87A4D706AD098F CRC64;

  Query Match             16.3%;  Score 128;  DB 1;  Length 318;
  Best Local Similarity   23.5%;  Pred. No. 0.0016;
  Matches   38;  Conservative   34;  Mismatches   62;  Indels   28;  Gaps    8;

Qy          8 PSDXPVAHVVAN----PQAEGQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |  :| ||:  |    |    ::    | : |  | ::| : | : :| |  :| | :|:
Db        161 PEAQPFAHLTINAADIPSGSHKVSLSSWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYA 219

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLL-SAIXSPCQRETPEGAEAXPW---- 114
               : |:              |   :   | | :| :: ::|: |      :|   : |
Db        220 NICFRHH----------ETSGSVPADYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNS 269

Qy        115 ---YEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
                 :  | :|| |:| :|: :| ::: |  ||  :    |||
Db        270 EFHFYSINVGGFFKLRAGEEISVQVSNPSLLD-PDQDATYFG 310


RESULT 186
Q4TVR2_SHEEP
ID   Q4TVR2_SHEEP   PRELIMINARY;   PRT;   261 AA.
AC   Q4TVR2;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   CD40 ligand.
GN   Name=CD154;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Oledzka G., Li B., Stankiewicz M.;
RT   "Cloning and sequence analysis of sheep (Ovis aries) CD154.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; DQ054533; AAY46795.1; -; mRNA.
DR   SMR; Q4TVR2; 116-261.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR13978:SF4; TNF_5; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01702; CD40LIGAND.
DR   ProDom; PD008600; TNF_5; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   261 AA;  29274 MW;  751D6291F09AA41A CRC64;

  Query Match             16.2%;  Score 127;  DB 2;  Length 261;
  Best Local Similarity   26.9%;  Pred. No. 0.0016;
  Matches   43;  Conservative   29;  Mismatches   50;  Indels   38;  Gaps    7;

Qy         14 AHVV--ANPQAEGQLQWLNRRANALLANGVELRD-NQLVVPSEGLYLIYSQVLFXGQGCP 70
              |||:  |: :   |||  :    | :| | | :  || |  :| | ||:|| |:
Db        124 AHVISEASSKTTSVLQWAPKGYYTLSSNLVTLENGKQLAVKRQGFYYIYTQVTFC----- 178

Qy         71 STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAE----------AXP-WYEP 117
                          | : ::|    |:| | : :| |:|          ::|   :
Db        179 --------------SNREALNQAPFIASLCLK-SPSGSERILLRAANTHSSSKPCGQQS 222

Qy        118 IYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |:|||||:|::|  :   :  |  :    :|   ||:: |
Db        223 IHLGGVFELQQGASVFVNVTDPSQVSHG-TGFTSFGLLKL 261


RESULT 187
Q5ZK93_CHICK
ID   Q5ZK93_CHICK   PRELIMINARY;   PRT;   292 AA.
AC   Q5ZK93;
DT   23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT   23-NOV-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Hypothetical protein.
GN   ORFNames=RCJMB04_12e7;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CB; TISSUE=Bursa;
RA   Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA   Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA   Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT   "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT   genefunction analysis.";
RL   Genome Biol. 6:R6-R6(2005).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ720191; CAG31850.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   292 AA;  33163 MW;  6DB230493520l0DA CRC64;

  Query Match             16.2%;  Score 127;  DB 2;  Length 292;
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  Best Local Similarity   28.5%;  Pred. No. 0.0018;
  Matches   39;  Conservative   27;  Mismatches   47;  Indels   24;  Gaps    6;

Qy         30 NRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF-------XGQGC------PSTHVLL 76
              :|| :: | | ||| : :|||| | | |||| |       :  |       |   |
Db        162 SRRGHSPLYN-VELWNGELVVPQTGFYYIYSQTYFRFRENEDEDSGLLERIKNPKQLVQY 220

Qy         77 THTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEI 136
              : ::    :|  :: |: : :: |  :     :|:     || ||||||:: ||:   :
Db        221 IYKLT----NYPDPILLMKSARTSCWSK-----KAEYGLYSIYQGGVFQLKREDRIFVSV 271

Qy        137 NRPDYLDFAESGQVYFG 153
             :  | :|  :    :||
Db        272 SNSDIVDMDKEAS-FFG 287


RESULT 188
TNF11_MOUSE
ID   TNF11_MOUSE    STANDARD;      PRT;   316 AA.
AC   O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
DT   24-JAN-2001, integrated into UniProtKB/Swiss-Prot.
DT   01-JAN-1998, sequence version 1.
DT   21-FEB-2006, entry version 62.
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) (CD254 antigen) [Contains: Tumor
DE   necrosis factor ligand superfamily member 11, membrane form; Tumor
DE   necrosis factor ligand superfamily member 11, soluble form].
GN   Name=Tnfsf11; Synonyms=Opgl, Rankl, Trance;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Hybridoma;
RX   MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Thymic lymphoma;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow;
RX   MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Bone marrow stroma;
RX   MEDLINE=98188248; PubMed=9520411; DOI=10.1073/pnas.95.7.3597;
RA   Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA   Mochizuki S., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
RA   Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT   "Osteoclast differentiation factor is a ligand for
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RT   to TRANCE/RANKL.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN   [5]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   STRAIN=129;
RX   MEDLINE=99214075; PubMed=10196481; DOI=10.1016/S0378-1119(99)00025-6;
RA   Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA   Ueda M., Higashio K.;
RT   "Cloning and characterization of the gene encoding mouse osteoclast
RT   differentiation factor.";
RL   Gene 230:121-127(1999).
RN   [6]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=21150053; PubMed=11250921; DOI=10.1210/en.142.4.1419;
RA   Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
RT   "Determination of three isoforms of the receptor activator of nuclear
RT   factor-kappaB ligand and their differential expression in bone and
RT   thymus.";
RL   Endocrinology 142:1419-1426(2001).
RN   [7]
RP   PROTEIN SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.
RX   MEDLINE=99240759; PubMed=10224132; DOI=10.1074/jbc.274.19.13613;
RA   Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,
RA   Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
RT   "Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha)-
RT   converting enzyme-like protease in shedding of TRANCE, a TNF family
RT   member involved in osteoclastogenesis and dendritic cell survival.";
RL   J. Biol. Chem. 274:13613-13618(1999).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.
RX   MEDLINE=21464816; PubMed=11581298;
RA   Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;
RT   "Crystal structure of the TRANCE/RANKL cytokine reveals determinants
RT   of receptor-ligand specificity.";
RL   J. Clin. Invest. 108:971-979(2001).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
RX   MEDLINE=21839021; PubMed=11733492; DOI=10.1074/jbc.M106525200;
RA   Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;
RT   "Crystal structure of the extracellular domain of mouse RANK ligand at
RT   2.2-A resolution.";
RL   J. Biol. Chem. 277:6631-6636(2002).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC       TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC       Augments the ability of dendritic cells to stimulate naive T-cell
CC       proliferation. May be an important regulator of interactions
CC       between T cells and dendritic cells and may play a role in the
CC       regulation of the T cell-dependent immune response. May also play
CC       an important role in enhanced bone-resorption in humoral
CC       hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC       (isoforms 1 and 2); Cytoplasmic (isoform 3).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=O35235-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O35235-2; Sequence=VSP_006449;
CC       Name=3;
CC         IsoId=O35235-3; Sequence=VSP_006448;
CC   -!- TISSUE SPECIFICITY: Highly expressed in thymus and lymph nodes,
CC       but not in nonlymphoid tissues and is abundantly expressed in T
CC       cells but not in B cells. A high level expression is also seen in
CC       the trabecular bone and lung.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC       by proteolytic processing. The cleavage may be catalyzed by
CC       ADAM17. A further shorter soluble form was observed.
CC   -!- DISEASE: Deficiency in Tnfsf11 results in failure to form lobulo-
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CC       alveolar mammary structures during pregnancy, resulting in death
CC       of newborns. Trance-deficient mice show severe osteopetrosis, with
CC       no osteoclasts, marrow spaces, or tooth eruption, and exhibit
CC       profound growth retardation at several skeletal sites, including
CC       the limbs, skull, and vertebrae and have marked chondrodysplasia,
CC       with thick, irregular growth plates and a relative increase in
CC       hypertrophic chondrocytes.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF013170; AAC71061.1; -; mRNA.
DR   EMBL; AF019048; AAB86812.1; -; mRNA.
DR   EMBL; AF053713; AAC40113.1; -; mRNA.
DR   EMBL; AB008426; BAA25425.1; -; mRNA.
DR   EMBL; AB022039; BAA36970.1; -; Genomic_DNA.
DR   EMBL; AB032771; BAA97257.1; -; mRNA.
DR   EMBL; AB032772; BAA97258.1; -; mRNA.
DR   EMBL; AB036798; BAA97259.1; -; mRNA.
DR   PDB; 1IQA; X-ray; A/B/C=157-316.
DR   PDB; 1JTZ; X-ray; X/Y/Z=156-316.
DR   PDB; 1S55; X-ray; A/B/C=161-316.
DR   Ensembl; ENSMUSG00000022015; Mus musculus.
DR   MGI; MGI:1100089; Tnfsf11.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0045453; P:bone resorption; IDA.
DR   GO; GO:0048535; P:lymph node development; TAS.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   GO; GO:0001503; P:ossification; IMP.
DR   GO; GO:0045672; P:positive regulation of osteoclast different. . .; IDA.
DR   GO; GO:0051260; P:protein homooligomerization; IDA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   3D-structure; Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Direct protein sequencing; Glycoprotein; Membrane;
KW   Receptor; Signal-anchor; Transmembrane.
FT   CHAIN         1    316       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT                                /FTId=PRO_0000034516.
FT   CHAIN       139    316       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form.
FT                                /FTId=PRO_0000034517.
FT   TOPO_DOM      1     48       Cytoplasmic (Potential).
FT   TRANSMEM     49     69       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     70    316       Extracellular (Potential).
FT   SITE        138    139       Cleavage.
FT   CARBOHYD    197    197       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    262    262       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC      1    117       Missing (in isoform 3).
FT                                /FTId=VSP_006448.
FT   VARSPLIC     14     44       SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (in
FT                                isoform 2).
FT                                /FTId=VSP_006449.
FT   CONFLICT     99     99       G -> D (in Ref. 2).
FT   CONFLICT    141    143       Missing (in Ref. 5).
FT   STRAND      164    169
FT   TURN        171    172
FT   STRAND      173    173
FT   STRAND      176    176
FT   STRAND      178    179
FT   STRAND      181    182
FT   STRAND      186    190
FT   TURN        191    192
FT   STRAND      194    201
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  Query Match           16.2%;  Score 127;  DB 1;  Length 316;
  Best Local Similarity  23.5%;  Pred. No. 0.002;
  Matches   38;  Conservative   34;  Mismatches   62;  Indels   28;  Gaps    8;

Qy          8 PSDXPVAHVVAN----PQAEGQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |  :| ||:  |    |     ::    | : |  | ::| : | : :| |  :| | :|:
Db        159 PEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYA 217

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLL-SAIXSPCQRETPEGAEAXPW---- 114
                : |:            |   :   | | :| :: ::|: |      :|   : |
Db        218 NICFRHH----------ETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNS 267

Qy        115 ---YEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
                :  | :|| |:| :|: :| ::: |  ||  :    |||
Db        268 EFHFYSINVGGFFKLRAGEEISIQVSNPSLLD-PDQDATYFG 308
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RESULT 189
Q3TWY5_MOUSE
ID   Q3TWY5_MOUSE   PRELIMINARY;   PRT;   316 AA.
AC   Q3TWY5;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Osteoclast-like cell cDNA, RIKEN full-length enriched library,
DE   clone:I420021N01 product:tumor necrosis factor (ligand) superfamily,
DE   member 11, full insert sequence.
GN   Name=Tnfsf11;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
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RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AK159498; BAE35131.1; -; mRNA.
DR   MGI; MGI:1100089; Tnfsf11.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0045453; P:bone resorption; IDA.
DR   GO; GO:0048535; P:lymph node development; TAS.
DR   GO; GO:0009887; P:organ morphogenesis; IMP.
DR   GO; GO:0001503; P:ossification; IMP.
DR   GO; GO:0045672; P:positive regulation of osteoclast different. . .; IDA.
DR   GO; GO:0051260; P:protein homooligomerization; IDA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   316 AA;  35003 MW;  8AF3825F92E0A786 CRC64;

  Query Match             16.2%;  Score 127;  DB 2;  Length 316;
  Best Local Similarity   23.5%;  Pred. No. 0.002;
  Matches   38;  Conservative   34;  Mismatches   62;  Indels   28;  Gaps    8;

Qy          8 PSDXPVAHVVAN----PQAEGQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |  :| ||:  |     |    ::    | : |  | ::| : | : :| |  :| | :|:
Db        159 PEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYA 217

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSY-QTXVNLL-SAIXSPCQRETPEGAEAXPW---- 114
                : |:              |   :   | | :| :: ::|: |      :|   : |
Db        218 NICFRHH----------ETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNS 267

Qy        115 ---YEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
                 :  | :|| |:| :|: :| ::: |  ||  :    |||
Db        268 EFHPYSINVGGFFKLRAGEEISIQVSNPSLLD-PDQDATYFG 308
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RESULT 190
Q7T1F2_CHICK
ID   Q7T1F2_CHICK   PRELIMINARY;   PRT;   304 AA.
AC   Q7T1F2;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 16.
DE   Tumor necrosis factor related apoptosis inducing ligand.
GN   Name=TRAIL;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   PubMed=15240938; DOI=10.1292/jvms.66.643;
RA   Sayed A.A., Horiuchi H., Furusawa S., Matsuda H.;
RT   "Molecular Cloning and Characterization of Chicken Tumor Necrosis
RT   Factor (TNF)-Superfamily Ligands, CD30L and TNF-Related Apoptosis
RT   Inducing Ligand (TRAIL).";
RL   J. Vet. Med. Sci. 66:643-650(2004).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB114678; BAC79267.1; -; mRNA.
DR   HSSP; P50591; 1D2Q.
DR   Ensembl; ENSGALG00000009179; Gallus gallus.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   304 AA;  34659 MW;  DFC128B517747C96 CRC64;

  Query Match             16.1%;  Score 126.5;  DB 2;  Length 304;
  Best Local Similarity   25.4%;  Pred. No. 0.0021;
  Matches   43;  Conservative   36;  Mismatches   55;  Indels   35;  Gaps    8;

Qy          2 RSSSRTP----SDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYL 57
              : || :|    | : : | : : ::       :|| :: | | ||| : :|||| | |
Db        136 KRSSASPHNYLSYRGIGHKIHSWES-------SRRGHSFLYN-VELWNGELVVPQTGFYY 187

Qy         58 IYSQVLF-------XGQGC------PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRE 104
              ||||  |       :  |       |   |   : ::    :|  :: |: : :: |  :
Db        188 IYSQTYFRFRENEDEDSGLLERIKNPKQLVQYIYKLT----NYPDPILLMKSARTSCWSK 243

Qy        105 TPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
                :|:     :| |||||:: ||:   ::  | :|  :    :||
Db        244 -----KAEYGLYSVYQGGVFQLKREDRIFVSVSNSDIVDMDKEAS-FFG 286


RESULT 191
Q54A98_HUMAN
ID   Q54A98_HUMAN   PRELIMINARY;   PRT;   244 AA.
AC   Q54A98;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Receptor activator of nuclear factor kappa B ligand 3.
GN   Name=hRANKL 3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=14751235; DOI=10.1016/j.bbrc.2003.12.191;
RA   Suzuki J., Ikeda T., Kuroyama H., Seki S., Kasai M., Utsuyama M.,
RA   Tatsumi M., Uematsu H., Hirokawa K.;
RT   "Regulation of osteoclastogenesis by three human RANKL isoforms
RT   expressed in NIH3T3 cells.";
RL   Biochem. Biophys. Res. Commun. 314:1021-1027(2004).
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CC   ---------------------------------------------------------------------
DR   EMBL; AB064268; BAB79693.1; -; mRNA.
DR   SMR; Q54A98; 89-244.
DR   Ensembl; ENSG00000120659; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Receptor.
SQ   SEQUENCE   244 AA;  27690 MW;  C827590684B6B83C CRC64;

  Query Match             16.0%;  Score 126;  DB 2;  Length 244;
  Best Local Similarity   23.9%;  Pred. No. 0.0018;
  Matches   38;  Conservative   33;  Mismatches   60;  Indels   28;  Gaps    8;

Qy         11 XPVAHVVAN----PQAEGQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
              :| ||:  |    |    ::    | : |  | ::| :   : :|:|  :| | :|: :
Db         90 QPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 148

Qy         64 FXGQGCPSTHVLLTHTISRIAVSY-QTXVNLL-SAIXSPCQRETPEGAEAXPW------- 114
              |:              |   :|  | | :| :  ::|: |       :|   : |
Db        149 FRHH----------ETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFH 198

Qy        115 YEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
              :  | :|| |:| :|: :| |:: |  ||  :    |||
Db        199 FYSINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 236


RESULT 192
TNF11_HUMAN
ID   TNF11_HUMAN    STANDARD;      PRT;   317 AA.
AC   O14788; O14723; Q96Q17; Q9P2Q3;
DT   24-JAN-2001, integrated into UniProtKB/Swiss-Prot.
DT   01-JAN-1998, sequence version 1.
DT   07-FEB-2006, entry version 54.
DE   Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE   of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE   induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE   differentiation factor) (ODF) (CD254 antigen) [Contains: Tumor
DE   necrosis factor ligand superfamily member 11, membrane form; Tumor
DE   necrosis factor ligand superfamily member 11, soluble form].
GN   Name=TNFSF11; Synonyms=OPGL, RANKL, TRANCE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC   TISSUE=Bone marrow, and Peripheral blood;
RX   MEDLINE=98032977; PubMed=9367155; DOI=10.1038/36593;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
```

```
RL   Nature 390:175-179(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC   TISSUE=Lymph node;
RX   MEDLINE=98227661; PubMed=9568710; DOI=10.1016/S0092-8674(00)81569-X;
RA   Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA   Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA   Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA   Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA   Boyle W.J.;
RT   "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT   differentiation and activation.";
RL   Cell 93:165-176(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1; 2 AND 3).
RA   Ikeda T., Kuroyama H., Hirokawa K.;
RT   "Determination of human RANKL isoforms.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RC   TISSUE=Tongue;
RX   MEDLINE=20175237; PubMed=10708588; DOI=10.1006/bbrc.2000.2314;
RA   Nagai M., Kyakumoto S., Sato N.;
RT   "Cancer cells responsible for humoral hypercalcemia express mRNA
RT   encoding a secreted form of ODF/TRANCE that induces osteoclast
RT   formation.";
RL   Biochem. Biophys. Res. Commun. 269:532-536(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 73-317.
RC   TISSUE=Thymocyte;
RX   MEDLINE=97460112; PubMed=9312132; DOI=10.1074/jbc.272.40.25190;
RA   Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA   Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA   Choi Y.;
RT   "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT   that activates c-Jun N-terminal kinase in T cells.";
RL   J. Biol. Chem. 272:25190-25194(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
CC       TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC       Augments the ability of dendritic cells to stimulate naive T-cell
CC       proliferation. May be an important regulator of interactions
CC       between T cells and dendritic cells and may play a role in the
CC       regulation of the T cell-dependent immune response. May also play
CC       an important role in enhanced bone-resorption in humoral
CC       hypercalcemia of malignancy.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
CC       Secreted (isoform 2). A soluble form of isoform 1 arises by
CC       proteolytic processing (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=O14788-1; Sequence=Displayed;
CC       Name=2; Synonyms=SODF;
CC         IsoId=O14788-2; Sequence=VSP_006447;
CC       Name=3;
CC         IsoId=O14788-3; Sequence=VSP_006446;
CC   -!- TISSUE SPECIFICITY: Highest in the peripheral lymph nodes, weak in
CC       spleen, peripheral blood Leukocytes, bone marrow, heart, placenta,
CC       skeletal muscle, stomach and thyroid.
CC   -!- INDUCTION: Up-regulated by T cell receptor stimulation.
CC   -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC       by proteolytic processing (By similarity). The cleavage may be
CC       catalyzed by ADAM17.
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF019047; AAB86811.1; -; mRNA.
DR   EMBL; AF053712; AAC39731.1; -; mRNA.
DR   EMBL; AB064269; BAB79694.1; -; mRNA.
DR   EMBL; AB061227; BAB71768.1; -; mRNA.
DR   EMBL; AB064270; BAB79695.1; -; mRNA.
DR   EMBL; AB037599; BAA90488.1; -; mRNA.
DR   EMBL; BC074823; AAH74823.1; -; mRNA.
DR   EMBL; BC074890; AAH74890.1; -; mRNA.
DR   EMBL; AF013171; AAC51762.1; -; mRNA.
DR   HSSP; O35235; 1JTZ.
DR   SMR; O14788; 162-317.
DR   Ensembl; ENSG00000120659; Homo sapiens.
DR   HGNC; HGNC:11926; TNFSF11.
DR   MIM; 602642; gene.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   GO; GO:0030316; P:osteoclast differentiation; NAS.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; FALSE_NEG.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Alternative splicing; Cytokine; Developmental protein;
KW   Differentiation; Glycoprotein; Membrane; Receptor; Signal-anchor;
KW   Transmembrane.
FT   CHAIN         1    317       Tumor necrosis factor ligand superfamily
FT                                member 11, membrane form.
FT                                /FTId=PRO_0000034514.
FT   CHAIN       140    317       Tumor necrosis factor ligand superfamily
FT                                member 11, soluble form (By similarity).
FT                                /FTId=PRO_0000034515.
FT   TOPO_DOM      1     47       Cytoplasmic (Potential).
FT   TRANSMEM     48     68       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     69    317       Extracellular (Potential).
FT   SITE        139    140       Cleavage (By similarity).
FT   CARBOHYD    171    171       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    198    198       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC      1     73       Missing (in isoform 2).
FT                                /FTId=VSP_006447.
FT   VARSPLIC      1     47       Missing (in isoform 3).
FT                                /FTId=VSP_006446.
FT   CONFLICT    194    194       A -> G (in Ref. 6).
SQ   SEQUENCE   317 AA;  35478 MW;  766176446348097F CRC64;

  Query Match             16.0%;  Score 126;  DB 1;  Length 317;
  Best Local Similarity   23.9%;  Pred. No. 0.0025;
  Matches   38;  Conservative   33;  Mismatches   60;  Indels   28;  Gaps    8;
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Qy          11 XPVAHVVAN----PQAEGQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
               :| ||:  |    |    ::    | : |  | ::| :   : :|:|  :| | :|: :
Db         163 QPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221

Qy          64 FXGQGCPSTHVLLTHTISRIAVSY-QTXVNLL-SAIXSPCQRETPEGAEAXPW------- 114
               |:             |   :|  | | :|  :  ::|: |      :|   : |
Db         222 FRHH----------ETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFH 271

Qy         115 YEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
               :  | :|| |:| :|: :| |:: |  ||  :    |||
Db         272 FYSINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309


RESULT 193
Q5T9Y4_HUMAN
ID   Q5T9Y4_HUMAN   PRELIMINARY;   PRT;   317 AA.
AC   Q5T9Y4;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Tumor necrosis factor (Ligand) superfamily, member 11 (Fragment).
GN   Name=TNFSF11; ORFNames=RP11-86N24.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AL139382; CAI16926.1; -; Genomic_DNA.
DR   SMR; Q5T9Y4; 162-317.
DR   Ensembl; ENSG00000120659; Homo sapiens.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER     317    317
SQ   SEQUENCE   317 AA;  35478 MW;  766176446348097F CRC64;

  Query Match             16.0%;  Score 126;  DB 2;  Length 317;
  Best Local Similarity   23.9%;  Pred. No. 0.0025;
  Matches   38;  Conservative   33;  Mismatches   60;  Indels   28;  Gaps    8;

Qy          11 XPVAHVVAN----PQAEGQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 63
               :| ||:  |    |    ::    | : |  | ::| :   : :|:|  :| | :|: :
Db         163 QPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221

Qy          64 FXGQGCPSTHVLLTHTISRIAVSY-QTXVNLL-SAIXSPCQRETPEGAEAXPW------- 114
               |:             |   :|  | | :|  :  ::|: |      :|   : |
Db         222 FRHH----------ETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFH 271

Qy         115 YEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFG 153
               :  | :|| |:| :|: :| |:: |  ||  :    |||
Db         272 FYSINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309


RESULT 194
CD40L_PIG
ID   CD40L_PIG      STANDARD;      PRT;   261 AA.
AC   Q95MQ5;
DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   06-JUN-2002, sequence version 2.
DT   07-MAR-2006, entry version 32.
DE   CD40 ligand (CD40-L) (Tumor necrosis factor ligand superfamily member
DE   5) (CD154 antigen) [Contains: CD40 ligand, membrane form; CD40 ligand,
DE   soluble form].
GN   Name=CD40LG; Synonyms=CD40L, TNFSF5;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Spleen;
RA   Uenishi H.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 45-227.
RA   Han X., Tuch B.E.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC       proliferation in the absence of co-stimulus as well as IgE
CC       production in the presence of IL-4. Involved in immunoglobulin
CC       class switching (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB040443; BAB86593.1; -; mRNA.
DR   EMBL; AF263915; AAK58524.1; -; mRNA.
DR   HSSP; P29965; 1ALY.
DR   SMR; Q95MQ5; 116-261.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0005174; F:CD40 receptor binding; ISS.
DR   GO; GO:0042100; P:B cell proliferation; ISS.
DR   GO; GO:0006954; P:inflammatory response; ISS.
DR   GO; GO:0007159; P:leukocyte adhesion; ISS.
DR   GO; GO:0030168; P:platelet activation; ISS.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR13978:SF4; TNF_5; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01702; CD40LIGAND.
DR   ProDom; PD008600; TNF_5; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    261       CD40 ligand, membrane form.
FT                                /FTId=PRO_0000034492.
FT   CHAIN       113    261       CD40 ligand, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034493.
FT   TOPO_DOM      1     22       Cytoplasmic (Potential).
FT   TRANSMEM     23     43       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     44    240       Extracellular (Potential).
FT   SITE        112    113       Cleavage (By similarity).
FT   CARBOHYD    240    240       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    178    218       Potential.
SQ   SEQUENCE   261 AA;  28869 MW;  9700077334556C97 CRC64;

  Query Match             15.8%;  Score 124;  DB 1;  Length 261;
  Best Local Similarity   26.9%;  Pred. No. 0.003;
  Matches   43;  Conservative   27;  Mismatches   52;  Indels   38;  Gaps    7;

Qy          14 AHVV--ANPQAEGQLQWLNRRANALLANGVELRD-NQLVVPSEGLYLIYSQVLFXGQGCP 70
               |||:  |: :    |||  :    |  | | | :  || |  :|:| ||:|| |:
```

```
Db        124 AHVISEASSKTASVLQWAPKGYYTLSTNLVTLENGRQLAVKRQGIYYIYAQVTFC----- 178

Qy         71 STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAE-----------AXP-WYEP 117
                                  | : :      |:| | | :| |:|            ::|   :
Db        179 --------------SNRDAAGQAPFIASLCLR-SPSGSERILLRAANTHSSSKPCGQQS 222

Qy        118 IYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |:|||||:|::|  :   :  |  :    :|   ||:: |
Db        223 IHLGGVFELQPGASVFVNVTDPSQVSHG-TGFTSFGLLKL 261


RESULT 195
Q45NE6_HUMAN
ID   Q45NE6_HUMAN   PRELIMINARY;   PRT;   109 AA.
AC   Q45NE6;
DT   13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT   13-SEP-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Lymphotoxin alpha transcript variant 5 (Fragment).
GN   Name=LTA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood mononuclear cells activated with
RC   phytohemaglutinine;
RA   Smirnova A.S., Mine K.L., Ferreira-Silva K.C., Shulzhenko N.,
RA   Gerbase-DeLima M., Morgun A.;
RT   "Identification of new splice variants of the lymphotoxin alpha
RT   gene.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; DQ123824; AAZ32917.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002960; TNF_beta.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01236; TNFBETA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   109 AA;  11888 MW;  EC91130272D87EBF CRC64;

  Query Match             15.6%;  Score 123;  DB 2;  Length 109;
  Best Local Similarity   27.9%;  Pred. No. 0.0012;
  Matches   31;  Conservative   19;  Mismatches   37;  Indels   24;  Gaps    4;

Qy         11 XPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP 70
              :| ||:: :|  :  | |       | | :|  | :| |:||: |:| :|:|  :|
Db         14 KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQLPEDG---- 69

Qy         71 STHVLLTHTISRIAVSYQTXVNLLSAIXSP--CQRETPEGAEAXP--WYEP 117
                    :|| |          |:|:: |  |     |     :|  |: |
Db         70 ---------VSRAA-------GTLAALDVPRGCVPAHPGRPAIHPHRWHPP 104


RESULT 196
CD40L_CANFA
ID   CD40L_CANFA    STANDARD;      PRT;   260 AA.
AC   O97626;
DT   01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1999, sequence version 1.
DT   07-MAR-2006, entry version 41.
DE   CD40 ligand (CD40-L) (Tumor necrosis factor ligand superfamily member
DE   5) (CD154 antigen) [Contains: CD40 ligand, membrane form; CD40 ligand,
DE   soluble form].
GN   Name=CD40LG; Synonyms=CD40L, TNFSF5;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Hosie M.H., Willett B.J.;
RT   "Adjuvant properties of canine CD40L.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Yang S., Sim G.-K.;
RT   "Canine CD40 and CD40 ligand cDNA sequences.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC       proliferation in the absence of co-stimulus as well as IgE
CC       production in the presence of IL-4. Involved in immunoglobulin
CC       class switching (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF086711; AAD04375.1; -; mRNA.
DR   EMBL; AY333790; AAP86654.1; -; mRNA.
DR   HSSP; P29965; 1ALY.
DR   SMR; O97626; 115-260.
DR   Ensembl; ENSCAFG00000018945; Canis familiaris.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0005174; F:CD40 receptor binding; ISS.
DR   GO; GO:0042100; P:B cell proliferation; ISS.
DR   GO; GO:0006954; P:inflammatory response; ISS.
DR   GO; GO:0007159; P:leukocyte adhesion; ISS.
DR   GO; GO:0030168; P:platelet activation; ISS.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR13978:SF4; TNF_5; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01702; CD40LIGAND.
DR   ProDom; PD008600; TNF_5; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN         1    260       CD40 ligand, membrane form.
FT                                /FTId=PRO_0000034478.
FT   CHAIN       112    260       CD40 ligand, soluble form (By
FT                                similarity).
FT                                /FTId=PRO_0000034479.
FT   TOPO_DOM      1     22       Cytoplasmic (Potential).
FT   TRANSMEM     23     46       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     47    260       Extracellular (Potential).
FT   SITE        111    112       Cleavage (By similarity).
FT   CARBOHYD    239    239       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    177    217       Potential.
SQ   SEQUENCE   260 AA;  28688 MW;  604F69A19E98EB70 CRC64;

  Query Match             15.6%;  Score 123;  DB 1;  Length 260;
  Best Local Similarity   27.4%;  Pred. No. 0.0037;
  Matches   43;  Conservative   27;  Mismatches   55;  Indels   32;  Gaps    7;
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Qy          14 AHVV--ANPQAEGQLQWLNRRANALLANGVELRD-NQLVVPSEGLYLIYSQVLFXGQGCP 70
               |||:  |:      |:|  :    : :| | | :  || |  :||| :|:|| |:
Db         123 AHVISEASSNPASVLRWAPKGYYTISSNLVSLENGKQLAVKRQGLYYVYAQVTFCSNRAA 182

Qy          71 STHV-----LLTHTISRIAVSYQTXVNLLSAIXS-----PCQRETPEGAEAXPWYEPIYL 120
               |:       |  |: |       |:  || | :|     || :::           |:|
Db         183 SSQAPFVASLCLHSPS------GTERVLLRAASSRGSSKPCGQQS------------IHL 224

Qy         121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               ||||:| :|  :   :  |  :    :|   ||:: |
Db         225 GGVFELHPGASVFVNVTDPSQVSHG-TGFTSFGLLKL 260
```

RESULT 197
CD40L_FELCA
ID   CD40L_FELCA   STANDARD;   PRT;   260 AA.
AC   O97605;
DT   01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1999, sequence version 1.
DT   07-MAR-2006, entry version 40.
DE   CD40 ligand (CD40-L) (Tumor necrosis factor ligand superfamily member
DE   5) (CD154 antigen) [Contains: CD40 ligand, membrane form; CD40 ligand,
DE   soluble form].
GN   Name=CD40LG; Synonyms=CD40L, TNFSF5;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Thymus;
RA   Hosie M.J., Willett B.J.;
RT   "Adjuvant properties of feline CD154 (CD40 ligand).";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC   proliferation in the absence of co-stimulus as well as IgE
CC   production in the presence of IL-4. Involved in immunoglobulin
CC   class switching (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC   extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC   proteolytic processing (By similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; AF079105; AAD02954.1; -; mRNA.
DR   HSSP; P29965; 1ALY.
DR   SMR; O97605; 115-260.
DR   GO; GO:0016021; C:integral to membrane; ISS.
DR   GO; GO:0005174; F:CD40 receptor binding; ISS.
DR   GO; GO:0042100; P:B cell proliferation; ISS.
DR   GO; GO:0006954; P:inflammatory response; ISS.
DR   GO; GO:0007159; P:leukocyte adhesion; ISS.
DR   GO; GO:0030168; P:platelet activation; ISS.
DR   InterPro; IPR003263; TNF_5.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR13978:SF4; TNF_5; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01702; CD40LIGAND.
DR   ProDom; PD008600; TNF_5; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Glycoprotein; Membrane; Signal-anchor; Transmembrane.
FT   CHAIN   1   260   CD40 ligand, membrane form.
FT   /FTId=PRO_0000034482.
FT   CHAIN   112   260   CD40 ligand, soluble form (By
FT   similarity).
FT   /FTId=PRO_0000034483.
FT   TOPO_DOM   1   22   Cytoplasmic (Potential).
FT   TRANSMEM   23   46   Signal-anchor for type II membrane
FT   protein (Potential).
FT   TOPO_DOM   47   260   Extracellular (Potential).
FT   SITE   111   112   Cleavage (By similarity).
FT   CARBOHYD   239   239   N-linked (GlcNAc. . .) (Potential).
FT   DISULFID   177   217   Potential.
SQ   SEQUENCE   260 AA; 28727 MW; 349FA0391FB7B932 CRC64;

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  Query Match             15.6%;  Score 123;  DB 1;  Length 260;
  Best Local Similarity   27.2%;  Pred. No. 0.0037;
  Matches   41;  Conservative   28;  Mismatches   62;  Indels   20;  Gaps    5;

Qy          14 AHVV--ANPQAEGQLQWLNRRANALLANGVELRD-NQLVVPSEGLYLIYSQVLFXGQGCP 70
               |||:  |:      |||  :    : :| | | :  || |  :||| ||:|| |:
Db         123 AHVISEASSSTASVLQWAPKGYYTISSNLVTLENGKQLAVKRQGLYYIYAQVTFCSNREA 182

Qy          71 STHVLLTHTISRIAVSYQTXVNLLSA----IXSPCQRETPEGAEAXPWYEPIYLGGVFQL 126
               |:      ::   : |   :| | :|     : || :::           |:|||||:|
Db         183 SSQAPFIASLCLHSPSGSERVLLRAANARSSSKPCGQQS------------IHLGGVFEL 230

Qy         127 EXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                :|  :   :  |  :    :|   ||:: |
Db         231 HPGASVFVNVTDPSQVSHG-TGFTSFGLLKL 260
```

RESULT 198
Q2I7F6_ONCMY
ID   Q2I7F6_ONCMY   PRELIMINARY;   PRT;   291 AA.
AC   Q2I7F6;
DT   07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT   07-MAR-2006, sequence version 1.
DT   07-MAR-2006, entry version 1.
DE   TNF superfamily member 10-like protein.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Glenney G., Wiens G.D.;
RT   "Early Diversification of the Tumor Necrosis Factor Superfamily in
RT   Teleosts: Genomic Characterization and Expression Analysis.";
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---
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CC   ---
DR   EMBL; DQ218468; ABC84583.1; -; mRNA.
SQ   SEQUENCE   291 AA; 32189 MW; 07476C6402AC8FED CRC64;

```
  Query Match             15.6%;  Score 122.5;  DB 2;  Length 291;
  Best Local Similarity   23.8%;  Pred. No. 0.0049;
  Matches   45;  Conservative   32;  Mismatches   61;  Indels   51;  Gaps   10;

Qy           2 RSSSRTPSDXPVAHVV----------ANP--QAEGQ-LQWLNRRANALLANGVELRDN 46
               ::|||    :  |||             |:|  : :|| : |           | | |
Db         116 QASSR---PKVAAHVTGSFAPKAARGGASPGRRVQGQKISWWEGHKGLAFLQDVRLIDG 172

Qy          47 QLVVPSEGLYLIYSQVLFXGQGCPSTH-----------------VLLTHTISRIAVSY 87
               :|||| ||| ||:|  |:      ||                :| :   ::: ||
Db         173 ELVVPCPGLYYIYAQTYFR-----HTHPGGEEGEEEVEEEREQRGRPMLQYVYKKVS-SY 226

Qy          88 QTXVNLLSAIXSPC-QRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAE 146
               :: |:   :: |  |::      ::      : ||:| | :||||   ::    :|  |
Db         227 PVPILLMKTSRTSCWSRDSQFSLHSA------HQGGLFPLATGDRLLVTVSNASAIDMDE 280

Qy         147 SGQVYFGII 155
                  :|| :
```

```
Db        281 RSS-FFGAV 288


RESULT 199
Q4SKU4_TETNG
ID   Q4SKU4_TETNG   PRELIMINARY;   PRT;   285 AA.
AC   Q4SKU4;
DT   19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Chromosome undetermined SCAF14565, whole genome shotgun sequence.
GN   ORFNames=GSTENG00016551001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15496914; DOI=10.1038/nature03025;
RA   Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAE01014565; CAF98738.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   285 AA;  31211 MW;  77F921B17854A475 CRC64;

  Query Match            15.5%;  Score 121.5;  DB 2;  Length 285;
  Best Local Similarity   24.7%;  Pred. No. 0.0059;
  Matches   45;  Conservative   28;  Mismatches   62;  Indels   47;  Gaps    8;

Qy          7 TPSDXPVAHVV----------------ANPQAEGQ--LQWLNRRANALLANGVELRDNQ 47
              :|  :  |||                |  : :||  | |  ::  | | : |:| | :
Db        111 SPRPKVAAHVTGSFAPQLDRDEGGAPASAERRVQGQKILWWEGQKGLAFLQD-VQLVDGE 169

Qy         48 LVVPSEGLYLIYSQVLFXGQGCPSTHVL---------------LTHTISRIAVSYQTXV 91
              ||||  ||| :|:|  |:      || |               |   : :   ||  ::
Db        170 LVVPWPGLYYVYAQTYFR-----HTHSLEDAEEEGEEEGDRGRPLLQYVYKKVNSYPVPI 224

Qy         92 NLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEXGDRLSAEINRPDYLDFAESGQVY 151
               |:   :: |      |:: :      : ||:| | :|||   :     :|  |   :
Db        225 LLMKTSRTSC---WSRGSQFS--LHSAHQGGLFPLGSGDRLFVTVTNATAVDMDEKSS-F 278

Qy        152 FG 153
              ||
Db        279 FG 280


RESULT 200
Q90WP9_PLEPL
ID   Q90WP9_PLEPL   PRELIMINARY;   PRT;    88 AA.
AC   Q90WP9;
DT   01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT   01-DEC-2001, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   Tumour necrosis factor alpha (Fragment).
GN   Name=tnf-alpha;
OS   Pleuronectes platessa (Plaice).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Pleuronectidae; Pleuronectes.
OX   NCBI_TaxID=8262;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Laing K.J., Zou J.J., Secombes C.J.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AJ416943; CAC95226.1; -; mRNA.
DR   HSSP; P06804; 2TNF.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1      1
FT   NON_TER      88     88
SQ   SEQUENCE   88 AA;  9676 MW;  A8ED6CF0AB5F23E9 CRC64;

  Query Match            15.4%;  Score 121;  DB 2;  Length 88;
  Best Local Similarity   35.2%;  Pred. No. 0.0014;
  Matches   31;  Conservative   14;  Mismatches   31;  Indels   12;  Gaps    3;

Qy         54 GLYLIYSQVLF---------XGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQ-R 103
              ||| :||| |          :|:        ::| | | | |   : :|:||::| |
Db          1 GLYFVYSQASFSVSCSDDDAEGKDARGRLTSVSHRIWRYAESMGVKDSLMSAVRSACHVG 60

Qy        104 ETPEGA--EAXPWYEPIYLGGVFQLEXG 129
               | :|  : : ||  |||| |||| :|
Db         61 PTQDNAFRDGQGWYNAIYLGAVFQLNEG 88


Search completed: September 19, 2006, 18:05:01
Job time : 308 secs
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! FINDPATTERNS on pir:* allowing 0 mismatches

!        1 VRSSSRTPSD~(K)PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF~(K)GQGCPS
!        2 VNLLSAI~(K)SPCQRETPEGAEA~(K)PWYEPIYLGGVFQLE~(K)GDRLSAEINRPDYLDFAESGQVYFGIIAL


 Databases searched:
        NBRF, Release 80.0, Released on 31Dec2004, Formatted on 21Jun2005

     Total finds:              0
    Total length:     96,216,763
 Total sequences:        283,416
        CPU time:       03:53.96
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! FINDPATTERNS on uniprot:* allowing 0 mismatches

!         1 VRSSSRTPSD~(K)PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLF~(K)GQGCPS
!         2 VNLLSAI~(K)SPCQRETPEGAEA~(K)PWYEPIYLGGVFQLE~(K)GDRLSAEINRPDYLDFAESGQVYFGIIAL


 Databases searched:
        UNIPROT, Release 7.2, Released on 7Mar2006, Formatted on 7Mar2006

     Total finds:                0
    Total length:      925,015,592
 Total sequences:        2,849,598
        CPU time:          38:53.83
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! FINDPATTERNS on pir:* allowing 0 mismatches
!
!        1 VRSSSRTPSD(N,A,R,S,T,P,M,L)PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ
!        2 GQGCPSTHVLLTHTISRIAVSYQT(N,A,R,S,T,P,M,L)VNLLSAI(N,A,R,S,T,P,M,L)SPCQRETPEGAE
!        3 PWYEPIYLGGVFQLE(N,A,R,S,T,P,M,L)GDRLSAEINRPDYLDFAESGQVYFGIIAL


Databases searched:
       NBRF, Release 80.0, Released on 31Dec2004, Formatted on 21Jun2005

    Total finds:              0
   Total length:     96,216,763
Total sequences:        283,416
       CPU time:       05:37.98
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! FINDPATTERNS on uniprot:* allowing 0 mismatches

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!        1 VRSSSRTPSD(N,A,R,S,T,P,M,L)PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQ
!        2 GQGCPSTHVLLTHTISRIAVSYQT(N,A,R,S,T,P,M,L)VNLLSAI(N,A,R,S,T,P,M,L)SPCQRETPEGAE
!        3 PWYEPIYLGGVFQLE(N,A,R,S,T,P,M,L)GDRLSAEINRPDYLDFAESGQVYFGIIAL
```

Databases searched:
UNIPROT, Release 7.2, Released on 7Mar2006, Formatted on 7Mar2006

Total finds:	0
Total length:	925,015,592
Total sequences:	2,849,598
CPU time:	55:43.43

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 19, 2006, 09:03:18 ; Search time 4471 Seconds
(without alignments)
5890.853 Million cell updates/sec

Title: US-10-668-178-14
Perfect score: 471
Sequence: 1 gtcagatcatcttctcgaac.....actttgggatcattgccctg 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	447	94.9	702	14	AY421476	AY421476 Homo sapi
	2	445.4	94.6	702	14	AY421477	AY421477 Pan trogl
	3	445.4	94.6	1090	3	BM922481	BM922481 AGENCOURT
	4	444	94.3	641	5	CD685388	CD685388 EST1908 h
	5	377.4	80.1	1166	3	BM906148	BM906148 AGENCOURT
	6	361.2	76.7	702	10	DV799582	DV799582 est_t_tru
	7	326.4	69.3	829	2	BI908079	BI908079 603067163
	8	311.6	66.2	699	14	AY421478	AY421478 Mus muscu
	9	311.6	66.2	1638	6	AK155964	AK155964 Mus muscu
	10	311.6	66.2	1639	6	AK153800	AK153800 Mus muscu
	11	311.6	66.2	1640	6	AK153319	AK153319 Mus muscu
	12	303	64.3	569	2	BM255342	BM255342 517052 MA
	13	301.6	64.0	851	2	BI906520	BI906520 603063990
	14	300.8	63.9	749	2	BI907528	BI907528 603065671
c	15	294.2	62.5	501	13	CZ552051	CZ552051 DFA005 CH
	16	288.4	61.2	506	7	BF603144	BF603144 268577 MA
	17	271.8	57.7	1464	6	AK154223	AK154223 Mus muscu
	18	264.4	56.1	699	14	AG107303	AG107303 Pan trogl
	19	262.2	55.7	741	8	CR993406	CR993406 CR993406
	20	253.6	53.8	662	3	BM762686	BM762686 K-EST0043
	21	251.4	53.4	1081	3	BM922857	BM922857 AGENCOURT
	22	251.2	53.3	312	1	AA381742	AA381742 EST94911
	23	248.6	52.8	304	1	AA381586	AA381586 EST94694
	24	243	51.6	740	2	BI910312	BI910312 603068356
	25	242	51.4	665	1	AI253279	AI253279 ESTRB0004
	26	236.2	50.1	722	5	CK837301	CK837301 4062373 B
	27	215.6	45.8	1184	10	DV041399	DV041399 DAY10_02_
	28	205.2	43.6	241	1	AA371397	AA371397 EST83177
	29	203.4	43.2	858	9	DN948345	DN948345 AGENCOURT
	30	195.6	41.5	496	2	BM256426	BM256426 518793 MA
	31	195.2	41.4	835	9	CX756702	CX756702 AGENCOURT
	32	190.6	40.5	599	9	DA677133	DA677133 DA677133
c	33	182.8	38.8	1068	1	AL543083	AL543083 AL543083
c	34	180.4	38.3	313	11	AQ001135	AQ001135 CIT-HSP-2
	35	179.2	38.0	432	7	AW824779	AW824779 us07b08.y
	36	179.2	38.0	512	4	BX519887	BX519887 BX519887
	37	174.4	37.0	204	1	AA381637	AA381637 EST94763
c	38	171.6	36.4	315	11	AQ004745	AQ004745 CIT-HSP-2
	39	163.8	34.8	581	3	BP215875	BP215875 BP215875
	40	162.8	34.6	666	5	CJ137152	CJ137152 CJ137152
	41	150.8	32.0	216	1	AJ746780	AJ746780 AJ746780
c	42	150.2	31.9	216	1	AJ747097	AJ747097 AJ747097
	43	149.2	31.7	216	1	AJ746631	AJ746631 AJ746631
	44	149.2	31.7	216	1	AJ746769	AJ746769 AJ746769
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ALIGNMENTS

RESULT 1
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LOCUS AY421476 702 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens TNF gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY421476
VERSION AY421476.1 GI:39748338
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 702)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 702)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .702
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>702
/gene="TNF"
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ORIGIN

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  Query Match             94.9%;  Score 447;  DB 14;  Length 702;
  Best Local Similarity   96.8%;  Pred. No. 9.8e-95;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 2
AY421477
LOCUS       AY421477                 702 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Pan troglodytes TNF gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY421477
VERSION     AY421477.1  GI:39748339
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 702)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 702)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="Pan troglodytes"
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     gene            <1. .>702
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ORIGIN

  Query Match             94.6%;  Score 445.4;  DB 14;  Length 702;
  Best Local Similarity   96.6%;  Pred. No. 2.3e-94;
  Matches  455;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGACAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 3
BM922481
LOCUS       BM922481                 1090 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6626512 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5755513
            5', mRNA sequence.
ACCESSION   BM922481
VERSION     BM922481.1  GI:19372860
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1090)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12794  row: k  column: 02
            High quality sequence start: 10
            High quality sequence stop: 710.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
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                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             94.6%;  Score 445.4;  DB 3;  Length 1090;
  Best Local Similarity   96.6%;  Pred. No. 2.5e-94;
  Matches  455;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        398 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 457

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 517

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 577

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 637

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||    ||||||||||||||||||||    ||||||
Db        638 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 697

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        698 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 757

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        758 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 817

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        818 TATCTCGACTTTGGCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 868


RESULT 4
CD685388
LOCUS       CD685388                641 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST1908 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD685388
VERSION     CD685388.1  GI:32201298
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 641)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .641
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             94.3%;  Score 444;  DB 5;  Length 641;
  Best Local Similarity   96.8%;  Pred. No. 5e-94;
  Matches  453;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        174 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 233

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 293

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 353

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 413

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||    ||||||||||||||||||||    ||||||
Db        414 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 473

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        474 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 533

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        534 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 593

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCC 468
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Db        594 TATCTCGACTTTGGCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCC 641


RESULT 5
BM906148
LOCUS       BM906148                1166 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6621378 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590025
            5', mRNA sequence.
ACCESSION   BM906148
VERSION     BM906148.1  GI:19356527
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1166)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12363  row: k  column: 18
            High quality sequence start: 6
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .1166
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5590025"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
ORIGIN

  Query Match             80.1%;  Score 377.4;  DB 3;  Length 1166;
  Best Local Similarity   91.7%;  Pred. No. 2.7e-78;
  Matches  432;  Conservative    0;  Mismatches   36;  Indels    3;  Gaps    3;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        407 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 466

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 526

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 586

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        587 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 646

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||    |||||  ||||||||||||||    ||||||
Db        647 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAAACTCCTCTCTGCCATCAAGAGCCCC 706

Qy        301 TGCCAGA-GGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCT 359
              |||||||  |||||||||||||||||||||| | |   ||||||||||||||| |||||||
Db        707 TGCCAGAGGGGAGACCCCAGAGGGGGCTGAAGGCAAGCCCTGGTATGAGCCCCTCTATCT 766

Qy        360 GGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGA 419
              ||||||||  ||  |||||  |  ||  ||||||||| ||||||||| |||| ||||||
Db        767 GGGAGGGGCCTCCCCACTGGAAAAGGGGGACCGACTCCGCGCTGAGAT-AATCCGCCCGA 825

Qy        420 CTATCTCGACTTTG-CCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCC 469
              ||||||||||||| ||||||||||||||| | ||||||||   ||  ||
Db        826 ATATCTCGACTTTGCCCGAGTCTGGGCAGGGCCACTTTGGGGATCTTTGCC 876


RESULT 6
DV799582
LOCUS       DV799582                 702 bp    mRNA    linear   EST 23-NOV-2005
DEFINITION  est_t_truncatus2256 HML_TuTr_IL-2_PBL Tursiops truncatus cDNA, mRNA
            sequence.
ACCESSION   DV799582
VERSION     DV799582.1  GI:82652491
KEYWORDS    EST.
SOURCE      Tursiops truncatus (bottlenosed dolphin)
  ORGANISM  Tursiops truncatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
            Odontoceti; Delphinidae; Tursiops.
REFERENCE   1  (bases 1 to 702)
  AUTHORS   Mancia,A., Gefroh,H.A., Lundqvist,M.L., Romano,T.A., Almeida,J.S.,
            Chen,Y., McKillen,D.J., Trent,H.F., Wu,S. and Warr,G.W.
  TITLE     Construction and validation of T. truncatus immunospecific cDNA
            microarray at marinegenomics.org
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Annalaura Mancia
            Hollings Marine Lab
            Medical University of South Carolina
            Hollings Marine Lab, 331 Ft. Johnson Rd., Charleston, SC 29412, USA
            Tel: (843) 762 8962
            Fax: (843) 762 8737
            Email: mancia@musc.edu.
FEATURES             Location/Qualifiers
     source          1. .702
                     /organism="Tursiops truncatus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9739"
                     /tissue_type="PBL"
                     /cell_type="PBL"
                     /clone_lib="HML_TuTr_IL-2_PBL"
                     /note="Vector: pCR2.1TOPO; Site_1: GAATTC"
ORIGIN

  Query Match             76.7%;  Score 361.2;  DB 10;  Length 702;
  Best Local Similarity   85.5%;  Pred. No. 1.7e-74;
  Matches  402;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy          2 TCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCTC 61
              |||||||||||||   |||| | ||| ||  ||| ||||||||||||||||||  ||||
Db        230 TCAGATCATCTTCTAAAACCTCAAGTAACAAGCCCGTAGCCCATGTTGTAGCCAACCTCA 289

Qy         62 AAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCG 121
                || |||||||||||| |||||||||      |||||  ||||||||||||  |||
Db        290 GTACTCAGGGGCAGCTCCGGTGGCTGAACACATATGCCAACACCCTCCTGGCCAACAGCG 349

Qy        122 TGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCC 181
              || |||||  ||| ||||||||||||||||  | || || ||||||||||||||||||
Db        350 TGAAGCTGGAAGACAACCAGCTGGTGGTGCCGACGGATGGGCTGTACCTCATCTACTCCC 409

Qy        182 AGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATCA 241
              ||||||||||  |||||||||||||||| ||||||||  || ||||||||||||||||||
Db        410 AGGTCCTCTTCAGGGGCCAAGGCTGCCCTTCCACCCACTTGTTCCTCACCCACACCATCA 469

Qy        242 GCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCCT 301
              |||||||||| |||||||||| | ||   ||||||||||||||||||||  |||||  |
Db        470 GCCGCATCGCTGTCTCCTACCCGTCCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCTT 529

Qy        302 GCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTGG 361
              ||||||||||||  ||||||||||||||||||||  |||||||  |||||||||||  | ||
Db        530 GCCAGAGGGAGACGCCAGAGGGGGCTGAGGCCAAGCCCTGGTACGAGCCCATCTACCAGG 589

Qy        362 GAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACT 421
              ||||||||||||||||||||  |||||  |||||||  ||||||||||  | ||||||||
Db        590 GAGGGGTCTTCCAGCTGGAGAAGGGTGATCGACTCAGTGCTGAGATCAACCTGCCCGACT 649

Qy        422 ATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              ||||  ||||||||  ||||||||||||||||||||||||||||||||||
Db        650 ATCTGGACTTTGCTAAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 7
BI908079
LOCUS       BI908079                 829 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603067163F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216438 5',
            mRNA sequence.
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ACCESSION   BI908079
VERSION     BI908079.1  GI:16170982
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 829)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11543  row: m  column: 15
            High quality sequence stop: 701.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5216438"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             69.3%;  Score 326.4;  DB 2;  Length 829;
  Best Local Similarity   91.2%;  Pred. No. 2.7e-66;
  Matches  392;  Conservative    0;  Mismatches   31;  Indels    7;  Gaps    4;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        399 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 458

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 518

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 578

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        579 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 638

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||
Db        639 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 698

Qy        301 TGCCA-GAGGGAGACCCCA-GAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATC 358
              |||||  ||||||||||||| ||||||||||||||    |||||||||||| ||||| ||
Db        699 TGCCACGAGGGAGACCCCATGAGGGGGCTGAGGCCACGCCCTGGTATGAGCTCATCTCTC 758

Qy        359 TGG-GAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGC----GCTGAGATCAATCG 413
              ||| || ||||||||||||||| |  || | |     | |    ||||||||| ||||
Db        759 TGGCGACGGGTCTTCCAGCTGCACGCCCGCGTGACCGACCTCAGCGGCTGAGATCCATCG 818

Qy        414 GCCCGACTAT 423
              ||||||||||
Db        819 GCCCGACTAT 828


RESULT 8
AY421478
LOCUS       AY421478                699 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Mus musculus TNF gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY421478
VERSION     AY421478.1  GI:39748340
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 699)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .699
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>699
                     /gene="TNF"
                     /locus_tag="HCM7570"
ORIGIN

  Query Match             66.2%;  Score 311.6;  DB 14;  Length 699;
  Best Local Similarity   80.4%;  Pred. No. 8.3e-63;
  Matches  378;  Conservative    0;  Mismatches   89;  Indels    3;  Gaps    1;

Qy          2 TCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCTC 61
              ||||||||||||||| ||   ||||||||  ||||||||||| || ||||||||||   |
Db        230 TCAGATCATCTTCTCAAAATTCGAGTGACAAGCCTGTAGCCCACGTCGTAGCAAACCACC 289

Qy         62 AAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCG 121
              |||  ||||  ||||||  |||||||||  ||  || |||||  ||||||||||||| |||
Db        290 AAGTGGAGGAGCAGCTGGAGTGGCTGAGCCAGCGCGCCAACGCCCTCCTGGCCAACGGCA 349

Qy        122 TGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCC 181
              ||||  ||  |  |||  |||||  ||  |||||||||  |  ||  ||  |||||||  |||||||||
Db        350 TGGATCTCAAAGACAACCAACTAGTGGTGCCAGCCGATGGGTTGTACCTTGTCTACTCCC 409

Qy        182 AGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATCA 241
              ||||  ||||||  |||  ||||||||||    ||  |  |  ||||||||||||||||||  |||
Db        410 AGGTTCTCTTCAAGGGACAAGGCTGCC---CCGACTACGTGCTCCTCACCCACACCGTCA 466

Qy        242 GCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCCT 301
              ||||  |  ||  ||||  ||||||      ||||||||||||||||||  ||   |||||||
Db        467 GCCGATTTGCTATCTCATACCAGGAGAAAGTCAACCTCCTCTCTGCCGTCAAGAGCCCCT 526
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Qy        302 GCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTGG 361
              |||  | ||| ||||| ||||||||||||  |   ||||||||||||||||| || ||||
Db        527 GCCCCAAGGACACCCCTGAGGGGGCTGAGCTCAAACCCTGGTATGAGCCCATATACCTGG 586

Qy        362 GAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACT 421
              |||| ||||||||||||||||  || |||| ||||||||||||| |||||| |||| | |
Db        587 GAGGAGTCTTCCAGCTGGAGAAGGGGGACCAACTCAGCGCTGAGGTCAATCTGCCCAAGT 646

Qy        422 ATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |  | ||||||||| ||||| ||||||||||||||||||  ||||||| |||
Db        647 ACTTAGACTTTGCGGAGTCCGGGCAGGTCTACTTTGGAGTCATTGCTCTG 696
```

RESULT 9
AK155964
LOCUS AK155964 1638 bp mRNA linear HTC 21-SEP-2005
DEFINITION Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830002F15 product:tumor necrosis factor, full insert sequence.
ACCESSION AK155964
VERSION AK155964.1 GI:74215094
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
CONSRTM RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
PUBMED 11217851
REFERENCE 5
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,

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            Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE     The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)
  PUBMED    16141072
REFERENCE   7
  AUTHORS   Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
            Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
            Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
            Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
            Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
            Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
            Wahlestedt,C.
  CONSRTM   RIKEN Genome Exploration Research Group
  TITLE     Antisense transcription in the mammalian transcriptome
  JOURNAL   Science 309 (5740), 1564-1566 (2005)
  PUBMED    16141073
REFERENCE   8  (bases 1 to 1638)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
            Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
            Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
            Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
            Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .1638
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                     /mol_type="mRNA"
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                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
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                     EQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQVLFKGQGCPDYVLLTHTVSR
                     FAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPK
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                     /note="putative"
     polyA_site      1638

  Query Match             66.2%;  Score 311.6;  DB 6;  Length 1638;
  Best Local Similarity   80.4%;  Pred. No. 9.1e-63;
  Matches  378;  Conservative    0;  Mismatches   89;  Indels    3;  Gaps    1;

Qy          2 TCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCTC 61
              ||||||||||||||| ||   ||||||||  |||||||||||| || ||||||||||  |
Db        404 TCAGATCATCTTCTCAAAATTCGAGTGACAAGCCTGTAGCCCACGTCGTAGCAAACCACC 463

Qy         62 AAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCG 121
              |||  |||| |||||  |||||||||  ||   || |||||  |||||||||||||| |||
Db        464 AAGTGGAGGAGCAGCTGGAGTGGCTGAGCCAGCGCGCCAACGCCCTCCTGGCCAACGGCA 523

Qy        122 TGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCC 181
              ||||  ||  | |||  |||||  ||  |||||||||  |  ||  ||   |||||||   |||||||||
Db        524 TGGATCTCAAAGACAACCAACTAGTGGTGCCAGCCGATGGGTTGTACCTTGTCTACTCCC 583

Qy        182 AGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATCA 241
              ||||  ||||||   |||  ||||||||||    ||   |  |  ||||||||||||||||||  |||
Db        584 AGGTTCTCTTCAAGGGACAAGGCTGCC---CCGACTACGTGCTCCTCACCCACACCGTCA 640

Qy        242 GCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCCT 301
              ||||  |  ||  ||||  ||||||       ||||||||||||||||||  ||   |||||||
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Qy        302 GCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTGG 361
              |||  | |||  |||||  ||||||||||||   |   ||||||||||||||||||  || ||||
Db        701 GCCCCAAGGACACCCCTGAGGGGGCTGAGCTCAAACCCTGGTATGAGCCCATATACCTGG 760

Qy        362 GAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACT 421
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Qy        422 ATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        821 ACTTAGACTTTGCGGAGTCCGGGCAGGTCTACTTTGGAGTCATTGCTCTG 870


RESULT 10
AK153800
LOCUS       AK153800               1639 bp    mRNA    linear   HTC 21-SEP-2005
DEFINITION  Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A630097B05 product:tumor necrosis factor, full
            insert sequence.
ACCESSION   AK153800
VERSION     AK153800.1  GI:74149061
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  PUBMED    10349636
REFERENCE   2
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            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  PUBMED    11076861
REFERENCE   4
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AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
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CONSRTM FANTOM Consortium
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1639)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
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Qy        122 TGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCC 181
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Db        643 GCCGATTTGCTATCTCATACCAGGAGAAAGTCAACCTCCTCTCTGCCGTCAAGAGCCCCT 702

Qy        302 GCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTGG 361
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Qy        422 ATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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RESULT 11
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DEFINITION  Mus musculus bone marrow macrophage cDNA, RIKEN full-length
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            full insert sequence.
ACCESSION   AK153319
VERSION     AK153319.1  GI:74142270
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
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            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
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            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
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            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
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            Rogers,J., Birney,E. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
```

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
PUBMED 12466851
REFERENCE 6
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
CONSRTM FANTOM Consortium
TITLE The transcriptional landscape of the mammalian genome
JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
CONSRTM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1640)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers
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Query Match 66.2%; Score 311.6; DB 6; Length 1640;
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Matches 378; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

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Qy         62 AAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCG 121
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Db        466 AAGTGGAGGAGCAGCTGGAGTGGCTGAGCCAGCGCGCCAACGCCCTCCTGGCCAACGGCA 525

Qy        122 TGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCC 181
              |||| || | ||| ||||| || |||||||||| | || ||  |||||||  |||||||||
Db        526 TGGATCTCAAAGACAACCAACTAGTGGTGCCAGCCGATGGGTTGTACCTTGTCTACTCCC 585

Qy        182 AGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATCA 241
              |||| ||||||  ||| ||||||||||   ||  | | ||||||||||||||||||| |||
Db        586 AGGTTCTCTTCAAGGGACAAGGCTGCC---CCGACTACGTGCTCCTCACCCACACCGTCA 642

Qy        242 GCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCCT 301
              ||||  | ||  |||| ||||||       ||||||||||||||||||| ||   |||||||
Db        643 GCCGATTTGCTATCTCATACCAGGAGAAAGTCAACCTCCTCTCTGCCGTCAAGAGCCCCT 702

Qy        302 GCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTGG 361
              |||  | ||| ||||| ||||||||||||  |   |||||||||||||||||| || ||||
Db        703 GCCCCAAGGACACCCCTGAGGGGGCTGAGCTCAAACCCTGGTATGAGCCCATATACCTGG 762

Qy        362 GAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACT 421
              |||| ||||||||||||||||  || |||| |||||||||||| |||||| |||| | |
Db        763 GAGGAGTCTTCCAGCTGGAGAAGGGGGACCAACTCAGCGCTGAGGTCAATCTGCCCAAGT 822

Qy        422 ATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |  | ||||||| ||||| ||||||||||||||||  |||||| |||
Db        823 ACTTAGACTTTGCGGAGTCCGGGCAGGTCTACTTTGGAGTCATTGCTCTG 872
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RESULT 12
BM255342
LOCUS       BM255342                569 bp    mRNA    linear   EST 17-DEC-2001
DEFINITION  517052 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM255342
VERSION     BM255342.1  GI:17890941
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 116  row: M  column: 23
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 3BOV"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from marrow, alveolar
                     macrophage, ovary, fetal semitendonosus muscle, and fetal
                     longissimus muscle."
ORIGIN

  Query Match             64.3%;  Score 303;  DB 2;  Length 569;
  Best Local Similarity   81.4%;  Pred. No. 8.7e-61;
  Matches  351;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy         41 CCCATGTTGTAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCA 100
              |||    |  |||  ||    |  ||  |||||||||||| ||||  | ||      ||||
Db         30 CCCTCCCTCCAGCCGACATCAACTCTCCGGGGCAGCTCCGGTGGTGGGACTCGTATGCCA 89

Qy        101 ATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGG 160
              ||||||||  |||||||  ||  |||  ||||   |||  ||||||||||||||||||  | || |
Db         90 ATGCCCTCATGGCCAACGGTGTGAAGCTGTAAGACAACCAGCTGGTGGTGCCTGCTGACG 149

Qy        161 GCCTGTACCTCATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATG 220
              | ||  |||||||||||||| ||||||||||||   |||||||||||||| |||||||
Db        150 GGCTTTACCTCATCTACTCACAGGTCCTCTTCAGGGGCCAAGGCTGCCCTTCCACCCCCT 209

Qy        221 TGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCC 280
              || ||||||||||||||||||||||||||| || ||||||||||||||   ||||||  |||
Db        210 TGTTCCTCACCCACACCATCAGCCGCATTGCAGTCTCCTACCAGACCAAGGTCAACATCC 269

Qy        281 TCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCT 340
              | |||||||||   |||||  |||||  |||||||||||||||  ||||||||||   ||||
Db        270 TGTCTGCCATCAAGAGCCCTTGCCACAGGGAGACCCCAGAGTGGGCTGAGGCCAAGCCCT 329

Qy        341 GGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCG 400
              |||||||  ||||||||  |  ||||||  ||||||||||||||||   ||  ||  ||  |||||  |
Db        330 GGTATGAACCCATCTACCAGGGAGGAGTCTTCCAGCTGGAGAAGGGAGATCGCCTCAGTG 389

Qy        401 CTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGA 460
              ||||||||||  |  |||  ||||||  ||  ||||  ||||||||||||||||||||||||||||||
Db        390 CTGAGATCAACCTGCCGGACTACCTGGACTATGCCGAGTCTGGGCAGGTCTACTTTGGGA 449

Qy        461 TCATTGCCCTG 471
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Db        450 TCATCGCCCTG 460


RESULT 13
BI906520
LOCUS       BI906520                851 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603063990F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213134 5',
            mRNA sequence.
ACCESSION   BI906520
VERSION     BI906520.1  GI:16169261
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 851)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11535  row: c  column: 23
            High quality sequence stop: 836.
FEATURES             Location/Qualifiers
     source          1. .851
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5213134"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             64.0%;  Score 301.6;  DB 2;  Length 851;
  Best Local Similarity   88.6%;  Pred. No. 1.9e-60;
  Matches  396;  Conservative    0;  Mismatches   40;  Indels   11;  Gaps    6;

Qy         34 CCTGTAGCCCATGTTGTAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 93
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Db        364 CCTCTCTCCCTCCCTCCAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 423

Qy         94 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 153
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 483

Qy        154 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCC 213
                |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        484 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCC 543

Qy        214 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCC-TACCAGACCCGCGT 272
                |||||||||||||||  |||||||||||||||||||||||||||||||||||||||  ||
Db        544 ACCCATGTGCTCCTCANCCACACCATCAGCCGCATCGCCGTCTCCTTACCAGACCAAGGT 603

Qy        273 CAACCTCCTCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGC 332
                |||||||||||||||||    |||||||||||||||||||||||||||||||||||      |
Db        604 CAACCTCCTCTCTGCCATCAAGAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGGCTGAGT 663

Qy        333 CC----TCCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGG-- 386
                |    |||  |  ||||||||||||||||||||||||||||||||||||||||  ||
Db        664 GCCAAGCCCCTGGTATTGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGAAGGGGT 723

Qy        387 TGACCGACTCAGCGCT--GAGATCAATC-GGCCCGACTATCTCGAC-TTTGCCGAGTCTG 442
                ||||||||||||||   |||||||||| ||||||||||||||||| ||||||||||||
Db        724 GACCCGACTCAGCGCTTGAAGATCAATCGGGCCCGACTATCTCGACTTTTGCCGAGTCTG 783

Qy        443 GGCAGGTCTACTTTGGGATCATTGCCC 469
                |||||||||||||||||||  ||  ||
Db        784 GGCAGGTCTACTTTGGGATCCTTTGCC 810


RESULT 14
BI907528
LOCUS       BI907528                749 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603065671F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214905 5',
            mRNA sequence.
ACCESSION   BI907528
VERSION     BI907528.1  GI:16170362
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 749)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11539  row: m  column: 18
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match           63.9%;  Score 300.8;  DB 2;  Length 749;
  Best Local Similarity   94.6%;  Pred. No. 2.9e-60;
  Matches  333;  Conservative    0;  Mismatches   17;  Indels    2;  Gaps    2;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        399 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 458

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 518

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 578

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCA-ACCATC 637

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||   ||||| |||||||||| ||||   ||||||
Db        638 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAAGCTCCTCTCTGACATCAAGAGCCCC 697

Qy        301 TGCCAGAGGGAGACCCCAGA-GGGGGCTGAGGCCCTCCCCTGGTATGAGCCC 351
              |||||||||||||||||||| ||||||||||||    |||||||||| ||
Db        698 TGCCAGAGGGAGACCCCAGAGGGGGGCTGAGGCCAAGGCCTGGTATGAGGCC 749


RESULT 15
CZ552051/c
LOCUS       CZ552051                501 bp    DNA     linear   GSS 20-OCT-2005
DEFINITION  DFA005 CHORI-241 Equus caballus genomic clone 020C09, genomic
            survey sequence.
ACCESSION   CZ552051
VERSION     CZ552051.1  GI:77950056
KEYWORDS    GSS.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Tallmadge,R.L., Lear,T.L. and Antczak,D.F.
  TITLE     Genomic characterization of MHC class I genes of the horse
  JOURNAL   Immunogenetics 57 (10), 763-774 (2005)
   PUBMED   16220348
COMMENT     Contact: Tallmadge RL
            Baker Institute for Animal Health
            College of Veterinary Medicine, Cornell University
            Hungerford Hill Rd, Ithaca, NY 14853, USA
            Tel: 607 256 5621
            Fax: 607 256 5608
            Email: rlt8@cornell.edu
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="Equus caballus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9796"
                     /clone="020C09"
                     /sex="male"
                     /cell_type="neutrophils"
                     /clone_lib="CHORI-241"
                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

  Query Match           62.5%;  Score 294.2;  DB 13;  Length 501;
  Best Local Similarity   87.1%;  Pred. No. 1e-58;
  Matches  323;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;
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Qy        101 ATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGG 160
              ||||||||||||||||||||||||  ||||| ||| |||||||||||||| ||||  || |
Db        501 ATGCCCTCCTGGCCAATGGCGTGTGGCTGACAGACAACCAGCTGGTGGTACCATTGGATG 442

Qy        161 GCCTGTACCTCATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATG 220
              | |||||||||||||||||||||||||||||    |||||||||||||| ||||||||||
Db        441 GGCTGTACCTCATCTACTCCCAGGTCCTCTTCAAAGGCCAAGGCTGCCCTTCCACCCATG 382

Qy        221 TGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCC 280
              |||||||||||||||||||||||| | || |||||||||| | ||   ||||||||||
Db        381 TGCTCCTCACCCACACCATCAGCCGCTTAGCTGTCTCCTACCCGTCCAAGGTCAACCTCC 322

Qy        281 TCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCT 340
              ||||||||||   ||||| ||||| | |||| |||| ||| ||||||| |||   ||||
Db        321 TCTCTGCCATCAAGAGCCCTTGCCACACGGAGTCCCCGGAGCAGGCTGAAGCCAAGCCCT 262

Qy        341 GGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCG 400
              |||||||||||||||| |||||||| |||  ||||||||||  ||||| |  |||||||
Db        261 GGTATGAGCCCATCTACCTGGGAGGAGTCAACCAGCTGGAGAAGGGTGATCACCTCAGCG 202

Qy        401 CTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGA 460
              |||||||||||| |||| ||||||||||||||| ||||| ||||||||||||||||||
Db        201 CTGAGATCAATCAGCCCAACTATCTCGACTTTGCGGAGTCCGGGCAGGTCTACTTTGGGA 142

Qy        461 TCATTGCCCTG 471
              ||||||||||
Db        141 TCATTGCCCTG 131
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
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Searched: 2330496 seqs, 876882855 residues

Total number of hits satisfying chosen parameters: 4660992

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	447	94.9	522	6	US-10-490-953-31	Sequence 31, Appl
	2	447	94.9	1643	7	US-11-359-721-6	Sequence 6, Appli
	3	447	94.9	1669	8	US-11-266-748A-29093	Sequence 29093, A
	4	419	89.0	604	6	US-10-834-268-2227	Sequence 2227, Ap
	5	402.8	85.5	3634	7	US-11-015-117-9	Sequence 9, Appli
c	6	402.8	85.5	22173	6	US-10-669-920-1175	Sequence 1175, Ap
c	7	402.8	85.5	184666	8	US-11-266-748A-23088	Sequence 23088, A
	8	402.8	85.5	4647455	6	US-10-641-321-205	Sequence 205, App
	9	332.4	70.6	558	7	US-11-015-117-21	Sequence 21, Appl
	10	325	69.0	10240	7	US-11-015-117-11	Sequence 11, Appl
	11	311.6	66.2	1644	7	US-11-015-117-12	Sequence 12, Appl
c	12	275.4	58.5	21781	6	US-10-669-920-1172	Sequence 1172, Ap
	13	186.2	39.5	1000	8	US-11-266-748A-220582	Sequence 220582,
	14	186.2	39.5	1000	8	US-11-266-748A-393633	Sequence 393633,
c	15	186.2	39.5	1000	8	US-11-266-748A-464679	Sequence 464679,
	16	54.4	11.5	1386	6	US-10-523-723-6	Sequence 6, Appli
	17	51.6	11.0	1000	8	US-11-266-748A-220583	Sequence 220583,
	18	51.6	11.0	1000	8	US-11-266-748A-393634	Sequence 393634,
c	19	51.6	11.0	1000	8	US-11-266-748A-464680	Sequence 464680,
	20	47.4	10.1	1272	6	US-10-953-349-35507	Sequence 35507, A
	21	47.4	10.1	1272	9	US-11-056-355B-10759	Sequence 10759, A
c	22	47.4	10.1	1297	9	US-11-218-305-24197	Sequence 24197, A
	23	47	10.0	1600	9	US-11-174-307B-753	Sequence 753, App
	24	47	10.0	1600	9	US-11-056-355B-19791	Sequence 19791, A
	25	46.8	9.9	2642	6	US-10-449-902-13009	Sequence 13009, A
	26	46	9.8	1515	9	US-11-218-305-5297	Sequence 5297, Ap
	27	46	9.8	2487	8	US-11-266-748A-29506	Sequence 29506, A
	28	46	9.8	5181	8	US-11-266-748A-31990	Sequence 31990, A
	29	45.8	9.7	1019	9	US-11-056-355B-9576	Sequence 9576, Ap
	30	45.8	9.7	1568	6	US-10-449-902-6298	Sequence 6298, Ap
	31	45.6	9.7	891	6	US-10-449-902-14008	Sequence 14008, A
	32	45.6	9.7	1961	6	US-10-449-902-20884	Sequence 20884, A
	33	45.6	9.7	5918	8	US-11-257-817-28	Sequence 28, Appl
c	34	45.4	9.6	2859	9	US-11-218-305-18862	Sequence 18862, A
c	35	45.2	9.6	1000	8	US-11-266-748A-295699	Sequence 295699,
	36	45.2	9.6	1000	8	US-11-266-748A-347128	Sequence 347128,
c	37	45.2	9.6	1000	8	US-11-266-748A-408665	Sequence 408665,
	38	45.2	9.6	1000	8	US-11-266-748A-479711	Sequence 479711,
	39	45.2	9.6	2626	6	US-10-449-902-14545	Sequence 14545, A
c	40	45	9.6	1278	6	US-10-374-780A-1323	Sequence 1323, Ap
	41	45	9.6	1431	9	US-11-056-355B-20078	Sequence 20078, A
	42	45	9.6	3217	9	US-11-218-305-20488	Sequence 20488, A
	43	44.8	9.5	1588	8	US-11-216-545-6363	Sequence 6363, Ap
	44	44.6	9.5	1352	6	US-10-953-349-33554	Sequence 33554, A
	45	44.6	9.5	1352	9	US-11-056-355B-2753	Sequence 2753, Ap

ALIGNMENTS

RESULT 1
US-10-490-953-31
; Sequence 31, Application US/10490953
; Publication No. US20060088908A1
; GENERAL INFORMATION:
; APPLICANT: SKERRA, ARNE
; APPLICANT: SCHLEHUBER, STEFFEN
; TITLE OF INVENTION: MUTEINS OF HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN AND
; TITLE OF INVENTION: RELATED PROTEINS
; FILE REFERENCE: 029029-0104
; CURRENT APPLICATION NUMBER: US/10/490,953
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10490
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/EP02/04223
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: PCT/EP01/11213
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(42)
; OTHER INFORMATION: Affinity tag Arg-Gly-Ser-His(6)-Gly(3)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (4)..(513)
; OTHER INFORMATION: fusion protein of tumor necrosis factor alpha and
; OTHER INFORMATION: affinity tag
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43)..(513)
; OTHER INFORMATION: mature tumor necrosis factor alpha
US-10-490-953-31

Query Match 94.9%; Score 447; DB 6; Length 522;
Best Local Similarity 96.8%; Pred. No. 5.1e-91;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db     .     43 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 102

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 162

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 222

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 282

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||||    ||||||||||||||||||||    ||||||
Db        283 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 342

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        343 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 402

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        403 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 462

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 513
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RESULT 2
US-11-359-721-6
; Sequence 6, Application US/11359721
; Publication No. US20060194234A1
; GENERAL INFORMATION:
; APPLICANT: Conn, Michael Morgan
; APPLICANT: Pelligrini, Mathew
; APPLICANT: Hwang, Seongwoo
; APPLICANT: Moon, Young-choon
; APPLICANT: Almstead, Neil
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA
; TITLE OF INVENTION: STRUCTURAL MOTIFS
; FILE REFERENCE: 10589-008
; CURRENT APPLICATION NUMBER: US/11/359,721
; CURRENT FILING DATE: 2006-02-21
; PRIOR APPLICATION NUMBER: US/10/475,026
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 60/282,966
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-359-721-6

Query Match 94.9%; Score 447; DB 7; Length 1643;
Best Local Similarity 96.8%; Pred. No. 6.3e-91;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        381 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 440

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 500

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 560

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 620

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||||    ||||||||||||||||||||    ||||||
Db        621 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 680

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        681 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 740

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        741 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 800

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 851
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RESULT 3
US-11-266-748A-29093
; Sequence 29093, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29093
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-29093

Query Match 94.9%; Score 447; DB 8; Length 1669;
Best Local Similarity 96.8%; Pred. No. 6.4e-91;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        398 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 457

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 517
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Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 577

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 637

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||    ||||||||||||||||||||    ||||||
Db        638 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 697

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        698 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 757

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        758 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 817

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 868


RESULT 4
US-10-834-268-2227
; Sequence 2227, Application US/10834268
; Publication No. US20060194211A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Burczynski, Michael E.
;  APPLICANT:  Twine, Natalie  C.
;  APPLICANT:  Trepicchio, William  L.
;  APPLICANT:  Strahs, Andrew
;  APPLICANT:  Immermann, Fred
;  APPLICANT:  Slonim, Donna K
;  APPLICANT:  Dorner, Andrew J.
;  TITLE OF INVENTION: Methods for Prognosis and Treatment of Solid Tumors
;  FILE REFERENCE: AM101080L2 (031896-013200)
;  CURRENT APPLICATION NUMBER: US/10/834,268
;  CURRENT FILING DATE:  2004-04-29
;  NUMBER OF SEQ ID NOS: 5315
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2227
;   LENGTH: 604
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-834-268-2227

  Query Match             89.0%;  Score 419;  DB 6;  Length 604;
  Best Local Similarity   96.6%;  Pred. No. 9.6e-85;
  Matches  428;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        162 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 221

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 281

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 341

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 401

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||    ||||||||||||||||||||    ||||||
Db        402 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 461

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        462 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 521

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        522 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 581

Qy        421 TATCTCGACTTTGCCGAGTCTGG 443
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Db        582 TATCTCGACTTTGCCGAGTCTGG 604


RESULT 5
US-11-015-117-9
; Sequence 9, Application US/11015117
; Publication No. US20060183199A1
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT:  SHARMA, SANJAI
;  APPLICANT:  CANTWELL, MARK
;  TITLE OF INVENTION: NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
;  TITLE OF INVENTION:  LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND
;  TITLE OF INVENTION:  TREATMENT OF MALIGNANCIES AND AUTOIMMUNE DISEASE
;  FILE REFERENCE: 041673-2119
;  CURRENT APPLICATION NUMBER: US/11/015,117
;  CURRENT FILING DATE:  2004-12-17
;  PRIOR APPLICATION NUMBER: 08/982,272
;  PRIOR FILING DATE: 1997-12-01
;  PRIOR APPLICATION NUMBER: 60/132,145
;  PRIOR FILING DATE: 1996-12-09
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 9
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-015-117-9

  Query Match             85.5%;  Score 402.8;  DB 7;  Length 3634;
  Best Local Similarity   95.0%;  Pred. No. 5.7e-81;
  Matches  416;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         34 CCTGTAGCCCATGTTGTAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 93
              ||| |  |||    |  ||||||||||||||||||||||||||||||||||||||||||||
Db       2152 CCTCTCTCCCTCCCTCCAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 2211

Qy         94 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2212 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 2271

Qy        154 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCC 213
              ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db       2272 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCC 2331

Qy        214 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db       2332 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCAAGGTC 2391

Qy        274 AACCTCCTCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 333
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       2392 AACCTCCTCTCTGCCATCAAGAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 2451

Qy        334 CTCCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGA 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db       2452 AAGCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGA 2511

Qy        394 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2512 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 2571

Qy        454 TTTGGGATCATTGCCCTG 471
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Db       2572 TTTGGGATCATTGCCCTG 2589


RESULT 6
US-10-669-920-1175/c
; Sequence 1175, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-066001
;  CURRENT APPLICATION NUMBER: US/10/669,920
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/004,113
;  PRIOR FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 10/052,482
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 09/997,722
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/034,650
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: US 10/085,117
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: US 10/087,192
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: US 10/322,696
;  PRIOR FILING DATE: 2002-12-17
;  NUMBER OF SEQ ID NOS: 1441
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1175
;   LENGTH: 22173
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-669-920-1175

  Query Match             85.5%;  Score 402.8;  DB 6;  Length 22173;
  Best Local Similarity   95.0%;  Pred. No. 8e-81;
  Matches  416;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         34 CCTGTAGCCCATGTTGTAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 93
              ||| |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db      15628 CCTCTCTCCCTCCCTCCAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 15569

Qy         94 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15568 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 15509

Qy        154 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCC 213
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db      15508 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCC 15449

Qy        214 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTC 273
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db      15448 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCAAGGTC 15389

Qy        274 AACCTCCTCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 333
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db      15388 AACCTCCTCTCTGCCATCAAGAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 15329

Qy        334 CTCCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGA 393
              ||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db      15328 AAGCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGA 15269

Qy        394 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15268 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 15209

Qy        454 TTTGGGATCATTGCCCTG 471
              ||||||||||||||||||
Db      15208 TTTGGGATCATTGCCCTG 15191


RESULT 7
US-11-266-748A-23088/c
; Sequence 23088, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23088
;   LENGTH: 184666
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-23088

  Query Match             85.5%;  Score 402.8;  DB 8;  Length 184666;
  Best Local Similarity   95.0%;  Pred. No. 1.2e-80;
  Matches  416;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         34 CCTGTAGCCCATGTTGTAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 93
              ||| |  |||    | ||||||||||||||||||||||||||||||||||||||||||||
Db     172948 CCTCTCTCCCTCCCTCCAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 172889

Qy         94 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172888 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 172829

Qy        154 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCC 213
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db     172828 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCC 172769

Qy        214 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTC 273
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     172768 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCAAGGTC 172709

Qy        274 AACCTCCTCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 333
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db     172708 AACCTCCTCTCTGCCATCAAGAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 172649

Qy        334 CTCCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGA 393
              ||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db     172648 AAGCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGA 172589

Qy        394 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172588 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 172529

Qy        454 TTTGGGATCATTGCCCTG 471
```

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                  ||||||||||||||||||
Db     172528 TTTGGGATCATTGCCCTG 172511


RESULT 8
US-10-641-321-205
; Sequence 205, Application US/10641321
; Publication No. US20060183128A1
; GENERAL INFORMATION:
;  APPLICANT: Berlin, Kurt
;  APPLICANT:  Olek, Alexander
;  APPLICANT:  Beck, Stephan
;  APPLICANT:  Hildmann, Thomas
;  APPLICANT:  Lewin, Jorn
;  APPLICANT:  Novik, Karen
;  TITLE OF INVENTION: Methods and Compositions for Differentiating Tissues or Cell Type
;  TITLE OF INVENTION:  Epigenetic Markers
;  FILE REFERENCE: 47675-49
;  CURRENT APPLICATION NUMBER: US/10/641,321
;  CURRENT FILING DATE:  2003-08-12
;  NUMBER OF SEQ ID NOS: 221
; SEQ ID NO 205
;   LENGTH: 4647455
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (4267840)
;   OTHER INFORMATION: unknown base
US-10-641-321-205

  Query Match             85.5%;  Score 402.8;  DB 6;  Length 4647455;
  Best Local Similarity   95.0%;  Pred. No. 2.2e-80;
  Matches  416;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          34 CCTGTAGCCCATGTTGTAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 93
               ||| |  |||    |  ||||||||||||||||||||||||||||||||||||||||||||
Db     2836540 CCTCTCTCCCTCCCTCCAGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGC 2836599

Qy          94 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 153
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2836600 CGGGCCAATGCCCTCCTGGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCA 2836659

Qy         154 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCC 213
               ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db     2836660 TCAGAGGGCCTGTACCTCATCTACTCCCAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCC 2836719

Qy         214 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTC 273
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     2836720 ACCCATGTGCTCCTCACCCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCAAGGTC 2836779

Qy         274 AACCTCCTCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 333
               ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db     2836780 AACCTCCTCTCTGCCATCAAGAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCC 2836839

Qy         334 CTCCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGA 393
                  ||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db     2836840 AAGCCCTGGTATGAGCCCATCTATCTGGGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGA 2836899

Qy         394 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 453
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2836900 CTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTAC 2836959

Qy         454 TTTGGGATCATTGCCCTG 471
               ||||||||||||||||||
Db     2836960 TTTGGGATCATTGCCCTG 2836977


RESULT 9
US-11-015-117-21
; Sequence 21, Application US/11015117
; Publication No. US20060183199A1
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT:  SHARMA, SANJAI
;  APPLICANT:  CANTWELL, MARK
;  TITLE OF INVENTION: NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
;  TITLE OF INVENTION:  LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND
;  TITLE OF INVENTION:  TREATMENT OF MALIGNANCIES AND AUTOIMMUNE DISEASE
;  FILE REFERENCE: 041673-2119
;  CURRENT APPLICATION NUMBER: US/11/015,117
;  CURRENT FILING DATE:  2004-12-17
;  PRIOR APPLICATION NUMBER: 08/982,272
;  PRIOR FILING DATE: 1997-12-01
;  PRIOR APPLICATION NUMBER: 60/132,145
;  PRIOR FILING DATE: 1996-12-09
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
;   LENGTH: 558
;   TYPE: DNA
;   ORGANISM: Bos sp.
US-11-015-117-21

  Query Match             70.6%;  Score 332.4;  DB 7;  Length 558;
  Best Local Similarity   81.7%;  Pred. No. 2.2e-65;
  Matches  384;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy           2 TCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCTC 61
               |||| || ||||||| | || | ||| ||  ||| |||||||| ||||||||  ||
Db          86 TCAGGTCCTCTTCTCAAGCCTCAAGTAACAAGCCGGTAGCCCACGTTGTAGCCGACATCA 145

Qy          62 AAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCG 121
               |  ||  |||||||||||| |||| | ||       |||||||||||| ||||||| || |
Db         146 ACTCTCCGGGGCAGCTCCGGTGGTGGGACTCGTATGCCAATGCCCTCATGGCCAACGGTG 205

Qy         122 TGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCC 181
               || |||||  ||| ||||||||||||||||||  | || || || ||||||||||||| |
Db         206 TGAAGCTGGAAGACAACCAGCTGGTGGTGCCTGCTGACGGGCTTTACCTCATCTACTCAC 265

Qy         182 AGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATCA 241
               ||||||||||  ||||||||||||||| |||||||   || ||||||||||||||||||
Db         266 AGGTCCTCTTCAGGGGCCAAGGCTGCCCTTCCACCCCCTTGTTCCTCACCCACACCATCA 325

Qy         242 GCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCCT 301
               ||||||| || ||||||||||||||   |||||| |||| |||||||||   |||||| |
Db         326 GCCGCATTGCAGTCTCCTACCAGACCAAGGTCAACATCCTGTCTGCCATCAAGAGCCCTT 385

Qy         302 GCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTGG 361
               |||| ||||||||||||||| ||||||||||   |||||||| || |||||||| | ||
Db         386 GCCACAGGGAGACCCCAGAGTGGGCTGAGGCCAAGCCCTGGTACGAACCCATCTACCAGG 445

Qy         362 GAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACT 421
               |||| ||||||||||||||||  || || || ||||| |||||||||| | ||| ||||
Db         446 GAGGAGTCTTCCAGCTGGAGAAGGGAGATCGCCTCAGTGCTGAGATCAACCTGCCGGACT 505

Qy         422 ATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
               | || |||| ||||||||| ||||||||||||||||||||||||||||||
Db         506 ACCTGGACTATGCCGAGTCCGGGCAGGTCTACTTTGGGATCATTGCCCTG 555


RESULT 10
US-11-015-117-11
; Sequence 11, Application US/11015117
; Publication No. US20060183199A1
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT:  SHARMA, SANJAI
;  APPLICANT:  CANTWELL, MARK
;  TITLE OF INVENTION: NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
;  TITLE OF INVENTION:  LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND
;  TITLE OF INVENTION:  TREATMENT OF MALIGNANCIES AND AUTOIMMUNE DISEASE
;  FILE REFERENCE: 041673-2119
;  CURRENT APPLICATION NUMBER: US/11/015,117
;  CURRENT FILING DATE:  2004-12-17
;  PRIOR APPLICATION NUMBER: 08/982,272
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;  PRIOR FILING DATE: 1997-12-01
;  PRIOR APPLICATION NUMBER: 60/132,145
;  PRIOR FILING DATE: 1996-12-09
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
;   LENGTH: 10240
;   TYPE: DNA
;   ORGANISM: Sus sp.
US-11-015-117-11

  Query Match             69.0%;  Score 325;  DB 7;  Length 10240;
  Best Local Similarity   85.7%;  Pred. No. 1.7e-63;
  Matches  361;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy          51 AGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCT 110
               ||| ||     |||| ||||| |||||||| |||| ||   |   ||||||||||||||
Db        8623 AGCCAATGTCAAAGCCGAGGGACAGCTCCAATGGCAGAGTGGGTATGCCAATGCCCTCCT 8682

Qy         111 GGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCT 170
               |||||| |||||| |||||| ||| ||||||||||||||||  |||| || ||||||||
Db        8683 GGCCAACGGCGTGAAGCTGAAAGACAACCAGCTGGTGGTGCCGACAGATGGGCTGTACCT 8742

Qy         171 CATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCAC 230
               |||||||||||||||||||||||  |||||||||||||||| |||||| | ||  |||||||
Db        8743 CATCTACTCCCAGGTCCTCTTCAGGGGCCAAGGCTGCCCTTCCACCAACGTTTTCCTCAC 8802

Qy         231 CCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCAT 290
               ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        8803 TCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCAT 8862

Qy         291 CGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCC 350
               |   |||||| |||||||||||||||||| |||||||| ||||||   |||||||| || ||
Db        8863 CAAGAGCCCTTGCCAGAGGGAGACCCCCGAGGGGGCCGAGGCCAAGCCCTGGTACGAACC 8922

Qy         351 CATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAA 410
               |||||| |||||||||||||||||||||||||  | ||| |||||||| || ||||||||
Db        8923 CATCTACCTGGGAGGGGTCTTCCAGCTGGAGAAGGATGATCGACTCAGTGCCGAGATCAA 8982

Qy         411 TCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCT 470
               | ||||||||||| |||||||| || |||||||||||||| ||||||||||||||||||
Db        8983 CCTGCCCGACTATCTGGACTTTGCTGAATCTGGGCAGGTCTATTTTGGGATCATTGCCCT 9042

Qy         471 G 471
               |
Db        9043 G 9043


RESULT 11
US-11-015-117-12
; Sequence 12, Application US/11015117
; Publication No. US20060183199A1
; GENERAL INFORMATION:
;  APPLICANT: KIPPS, THOMAS J.
;  APPLICANT:  SHARMA, SANJAI
;  APPLICANT:  CANTWELL, MARK
;  TITLE OF INVENTION: NOVEL EXPRESSION VECTORS CONTAINING ACCESSORY MOLECULE
;  TITLE OF INVENTION:  LIGAND GENES AND THEIR USE FOR IMMUNOMODULATION AND
;  TITLE OF INVENTION:  TREATMENT OF MALIGNANCIES AND AUTOIMMUNE DISEASE
;  FILE REFERENCE: 041673-2119
;  CURRENT APPLICATION NUMBER: US/11/015,117
;  CURRENT FILING DATE:  2004-12-17
;  PRIOR APPLICATION NUMBER: 08/982,272
;  PRIOR FILING DATE: 1997-12-01
;  PRIOR APPLICATION NUMBER: 60/132,145
;  PRIOR FILING DATE: 1996-12-09
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
;   LENGTH: 1644
;   TYPE: DNA
;   ORGANISM: Mus sp.
US-11-015-117-12

  Query Match             66.2%;  Score 311.6;  DB 7;  Length 1644;
  Best Local Similarity   80.4%;  Pred. No. 1.2e-60;
  Matches  378;  Conservative    0;  Mismatches   89;  Indels    3;  Gaps    1;

Qy           2 TCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCTC 61
               |||||||||||||||| ||   ||||||||  |||||||||||| || ||||||||||  |
Db         395 TCAGATCATCTTCTCAAAATTCGAGTGACAAGCCTGTAGCCCACGTCGTAGCAAACCACC 454

Qy          62 AAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGCG 121
               |||  |||| |||||| |||||||||| ||  || ||||| ||||||||||||||| |||
Db         455 AAGTGGAGGAGCAGCTGGAGTGGCTGAGCCAGCGCGCCAACGCCCTCCTGGCCAACGGCA 514

Qy         122 TGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCCC 181
               |||| || | ||| ||||| || ||||||||| | || ||  |||||||  |||||||||
Db         515 TGGATCTCAAAGACAACCAACTAGTGGTGCCAGCCGATGGGTTGTACCTTGTCTACTCCC 574

Qy         182 AGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATCA 241
               |||| ||||||  ||| ||||||||||   || | | |||||||||||||||||||| |||
Db         575 AGGTTCTCTTCAAGGGACAAGGCTGCC---CCGACTACGTGCTCCTCACCCACACCGTCA 631

Qy         242 GCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCCT 301
               ||||  | ||  |||| |||||       ||||||||||||||||| ||   |||||||
Db         632 GCCGATTTGCTATCTCATACCAGGAGAAAGTCAACCTCCTCTCTGCCGTCAAGAGCCCCT 691

Qy         302 GCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTGG 361
               |||  | ||| |||||  |||||||||||  |   ||||||||||||||||| || ||||
Db         692 GCCCCAAGGACACCCCTGAGGGGGCTGAGCTCAAACCCTGGTATGAGCCCATATACCTGG 751

Qy         362 GAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACT 421
               |||| ||||||||||||||||  || |||| |||||||||||| |||||| |||| | |
Db         752 GAGGAGTCTTCCAGCTGGAGAAGGGGGACCAACTCAGCGCTGAGGTCAATCTGCCCAAGT 811

Qy         422 ATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
               | | ||||||||  |||| ||||||||||||||||  |||||||  |||
Db         812 ACTTAGACTTTGCGGAGTCCGGGCAGGTCTACTTTGGAGTCATTGCTCTG 861


RESULT 12
US-10-669-920-1172/c
; Sequence 1172, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc S.
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 20366-066001
;  CURRENT APPLICATION NUMBER: US/10/669,920
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: US 10/004,113
;  PRIOR FILING DATE: 2001-10-23
;  PRIOR APPLICATION NUMBER: US 10/052,482
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 09/997,722
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/034,650
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: US 10/085,117
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: US 10/087,192
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 10/322,281
;  PRIOR FILING DATE: 2002-12-17
;  PRIOR APPLICATION NUMBER: US 10/322,696
;  PRIOR FILING DATE: 2002-12-17
;  NUMBER OF SEQ ID NOS: 1441
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1172
;   LENGTH: 21781
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-669-920-1172
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  Query Match           58.5%;  Score 275.4;  DB 6;  Length 21781;
  Best Local Similarity  80.0%;  Pred. No. 2.5e-52;
  Matches  337;  Conservative    0;  Mismatches   81;  Indels    3;  Gaps    1;

Qy         51 AGCAAACCCTCAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCT 110
              ||||||||  ||||  |||| ||||||  ||||||||| ||   || |||||  ||||||||
Db      16035 AGCAAACCACCAAGTGGAGGAGCAGCTGGAGTGGCTGAGCCAGCGCGCCAACGCCCTCCT 15976

Qy        111 GGCCAATGGCGTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCT 170
              ||||||  |||  |||| || | ||| |||||  || |||||||| | ||  ||   |||||||
Db      15975 GGCCAACGGCATGGATCTCAAAGACAACCAACTAGTGGTGCCAGCCGATGGGTTGTACCT 15916

Qy        171 CATCTACTCCCAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCAC 230
              ||||||||||||| ||||||  ||| |||||||||   ||  | | ||||||||||||
Db      15915 TGTCTACTCCCAGGTTCTCTTCAAGGGACAAGGCTGCC---CCGACTACGTGCTCCTCAC 15859

Qy        231 CCACACCATCAGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCAT 290
              |||||||  |||||||  | ||  |||| ||||||      ||||||||||||||||| |
Db      15858 CCACACCGTCAGCCGATTTGCTATCTCATACCAGGAGAAAGTCAACCTCCTCTCTGCCGT 15799

Qy        291 CGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCC 350
              |   ||||||||||  | ||| |||||  ||||||||||||  |   ||||||||||||||
Db      15798 CAAGAGCCCCTGCCCCAAGGACACCCCTGAGGGGGCTGAGCTCAAACCCTGGTATGAGCC 15739

Qy        351 CATCTATCTGGGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAA 410
              ||| || |||||||| ||||||||||||||||  || |||| |||||||||||||| ||||
Db      15738 CATATACCTGGGAGGAGTCTTCCAGCTGGAGAAGGGGGACCAACTCAGCGCTGAGGTCAA 15679

Qy        411 TCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCT 470
              || |||| | ||  | ||||||| |||| |||||||||||||||  ||||||| ||
Db      15678 TCTGCCCAAGTACTTAGACTTTGCGGAGTCCGGGCAGGTCTACTTTGGAGTCATTGCTCT 15619

Qy        471 G 471
              |
Db      15618 G 15618
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RESULT 13
US-11-266-748A-220582
; Sequence 220582, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 220582
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-220582

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  Query Match           39.5%;  Score 186.2;  DB 8;  Length 1000;
  Best Local Similarity  96.0%;  Pred. No. 1.2e-32;
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Qy        393 ACTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCAGGTCTA 452
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Qy        453 CTTTGGGATCATTGCCCTG 471
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Db        181 CTTTGGGATCATTGCCCTG 199
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RESULT 14
US-11-266-748A-393633
; Sequence 393633, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 393633
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-393633

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  Query Match           39.5%;  Score 186.2;  DB 8;  Length 1000;
  Best Local Similarity  96.0%;  Pred. No. 1.2e-32;
  Matches  191;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        273 CAACCTCCTCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGC 332
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Qy        453 CTTTGGGATCATTGCCCTG 471
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Db        181 CTTTGGGATCATTGCCCTG 199


RESULT 15
US-11-266-748A-464679/c
; Sequence 464679, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 464679
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-464679

  Query Match             39.5%;  Score 186.2;  DB 8;  Length 1000;
  Best Local Similarity   96.0%;  Pred. No. 1.2e-32;
  Matches  191;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        273 CAACCTCCTCTCTGCCATCGCCAGCCCCTGCCAGAGGGAGACCCCAGAGGGGGCTGAGGC 332
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Qy        453 CTTTGGGATCATTGCCCTG 471
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Job time : 513 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 19, 2006, 09:13:45 ; Search time 1463 Seconds
(without alignments)
3955.896 Million cell updates/sec

Title: US-10-668-178-14
Perfect score: 471
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	471	100.0	471	9	US-10-668-178-14	Sequence 14, Appl
2	456.6	96.9	471	7	US-10-354-985-12	Sequence 12, Appl
3	456.6	96.9	471	9	US-10-668-178-12	Sequence 12, Appl
4	447	94.9	699	3	US-09-982-308-1	Sequence 1, Appli
5	447	94.9	699	6	US-10-145-014-1	Sequence 1, Appli
6	447	94.9	701	12	US-10-523-328-2	Sequence 2, Appli
7	447	94.9	702	7	US-10-312-245-7	Sequence 7, Appli
8	447	94.9	702	9	US-10-825-282-17	Sequence 17, Appl
9	447	94.9	780	7	US-10-157-305A-19	Sequence 19, Appl
10	447	94.9	780	7	US-10-157-391-19	Sequence 19, Appl
11	447	94.9	780	7	US-10-157-096-19	Sequence 19, Appl
12	447	94.9	780	7	US-10-157-302-19	Sequence 19, Appl
13	447	94.9	780	7	US-10-157-215A-19	Sequence 19, Appl
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15	447	94.9	780	7	US-10-154-951B-19	Sequence 19, Appl
16	447	94.9	780	7	US-10-156-831-19	Sequence 19, Appl
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32	447	94.9	780	7	US-10-157-339-19	Sequence 19, Appl
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34	447	94.9	965	7	US-10-267-384-79	Sequence 79, Appl
35	447	94.9	1020	3	US-09-359-595-9	Sequence 9, Appli
36	447	94.9	1279	7	US-10-247-671-120	Sequence 120, App
37	447	94.9	1585	7	US-10-172-118-501	Sequence 501, App
38	447	94.9	1585	8	US-10-342-887-501	Sequence 501, App
39	447	94.9	1585	8	US-10-641-643-1329	Sequence 1329, Ap
40	447	94.9	1585	9	US-10-370-715B-19	Sequence 19, Appl
41	447	94.9	1643	6	US-10-272-411-4	Sequence 4, Appli
42	447	94.9	1643	6	US-10-218-547-3	Sequence 3, Appli
43	447	94.9	1643	6	US-10-272-328A-4	Sequence 4, Appli
44	447	94.9	1643	7	US-10-310-793-9	Sequence 9, Appli
45	447	94.9	1643	7	US-10-172-118-1901	Sequence 1901, Ap

ALIGNMENTS

RESULT 1
US-10-668-178-14
; Sequence 14, Application US/10668178
; Publication No. US20050013795A1
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
; APPLICANT: MAYUMI, Tadanori
; APPLICANT: TSUTSUMI, Yasuo
; APPLICANT: NAKAGAWA, Shinsaku
; APPLICANT: IKEGAMI, Hakuo
; TITLE OF INVENTION: Biologically-active conjugate
; FILE REFERENCE: MAYUMI2A
; CURRENT APPLICATION NUMBER: US/10/668,178
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: JP 83509/2002
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: JP 185387/2002
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic (DNA coding a variant protein of human tumor necrosis
; OTHER INFORMATION: factor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(471)
US-10-668-178-14

Query Match 100.0%; Score 471; DB 9; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.8e-123;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-354-985-12
; Sequence 12, Application US/10354985
; Publication No. US20040001802A1
; GENERAL INFORMATION:
; APPLICANT: MAYUMI, Tandanori et al.
; TITLE OF INVENTION: PHYSIOLOGICALLY ACTIVE COMPLEX
; FILE REFERENCE: MAYUMI=2
; CURRENT APPLICATION NUMBER: US/10/354,985
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: JP 083509/2002
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: JP 1185387/2002
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DNA encoding a variant protein of human tumor necrosis factor
US-10-354-985-12

Query Match 96.9%; Score 456.6; DB 7; Length 471;
Best Local Similarity 98.1%; Pred. No. 5.7e-119;
Matches 462; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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RESULT 3
US-10-668-178-12
; Sequence 12, Application US/10668178
; Publication No. US20050013795A1
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
; APPLICANT: MAYUMI, Tadanori
; APPLICANT: TSUTSUMI, Yasuo
; APPLICANT: NAKAGAWA, Shinsaku
; APPLICANT: IKEGAMI, Hakuo
; TITLE OF INVENTION: Biologically-active conjugate
; FILE REFERENCE: MAYUMI2A
; CURRENT APPLICATION NUMBER: US/10/668,178
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: JP 83509/2002
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: JP 185387/2002
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic (DNA coding a variant protein of human tumor necrosis
; OTHER INFORMATION: factor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(471)
US-10-668-178-12

Query Match 96.9%; Score 456.6; DB 9; Length 471;
Best Local Similarity 98.1%; Pred. No. 5.7e-119;
Matches 462; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 4
US-09-982-308-1
; Sequence 1, Application US/09982308
; Patent No. US20020106781A1
;   GENERAL INFORMATION:
;        APPLICANT: Dalie, Barbara
;                   Fan, Xuedong
;                   Lundell, Daniel
;                   Lunn, Charles
;                   Tan, Jimmy
;                   Zavodny, Paul
;        TITLE OF INVENTION: Mammalian TNF-a Convertases
;        NUMBER OF SEQUENCES: 21
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schering-Plough Corporation
;             STREET: 2000 Galloping Hill Road
;             CITY: Kenilworth
;             STATE: New Jersey
;             COUNTRY: USA
;             ZIP: 07033-0530
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: Apple Macintosh
;             OPERATING SYSTEM: Macintosh 8.1
;             SOFTWARE: Microsoft Word 6.0.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/982,308
;             FILING DATE: 17-Oct-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/156,163
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McLaughlin, Jaye P.
;             REGISTRATION NUMBER: 41,211
;             REFERENCE/DOCKET NUMBER: JB0601QB
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 908 298 5056
;             TELEFAX: 908 298 5388
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 699 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        FEATURE:
;             OTHER INFORMATION:  The residue at position -14 of the sequence
;             is a phenylanine in the Swiss-Prot sequence, Accession
;             Code Swiss-Prot P01375, and as a serine in the GenBank sequence,
;             Accession Number M10988.
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-982-308-1

  Query Match            94.9%;  Score 447;  DB 3;  Length 699;
  Best Local Similarity  96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||

Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||  ||||||
Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 5
US-10-145-014-1
; Sequence 1, Application US/10145014
; Publication No. US20020168755A1
; GENERAL INFORMATION:
;  APPLICANT: Dalie, Barbara
;  APPLICANT:  Fan, Xuedong
;  APPLICANT:  Lundell, Daniel
;  APPLICANT:  Lunn, Charles A.
;  APPLICANT:  Tan, Jimmy C.
;  APPLICANT:  Zavodny, Paul J.
;  TITLE OF INVENTION: Mammalian TNF-alpha Convertases
;  FILE REFERENCE: JB0601QD
;  CURRENT APPLICATION NUMBER: US/10/145,014
;  CURRENT FILING DATE:  2002-05-14
;  PRIOR APPLICATION NUMBER: 09/982,308
;  PRIOR FILING DATE: 2001-10-17
;  PRIOR APPLICATION NUMBER: 09/156,163
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 08/889,909
;  PRIOR FILING DATE: 1997-07-10
;  PRIOR APPLICATION NUMBER: 60/021,710
;  PRIOR FILING DATE: 1996-07-12
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 699
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-145-014-1

  Query Match            94.9%;  Score 447;  DB 6;  Length 699;
  Best Local Similarity  96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||

Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348
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Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||  ||||||
Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699
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RESULT 6
US-10-523-328-2
; Sequence 2, Application US/10523328
; Publication No. US20060078944A1
; GENERAL INFORMATION:
; APPLICANT: Kuai, Jun
; APPLICANT: Lin, Lih-Ling
; APPLICANT: Wooters, Joseph L.
; APPLICANT: Nickbarg, Elliot
; TITLE OF INVENTION: METHODS AND REAGENTS RELATING TO INFLAMMATION AND APOPTOSIS
; FILE REFERENCE: WYTH-P01-001
; CURRENT APPLICATION NUMBER: US/10/523,328
; CURRENT FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: 60/400,410
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 701
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-523-328-2

Query Match 94.9%; Score 447; DB 12; Length 701;
Best Local Similarity 96.8%; Pred. No. 3e-116;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        228 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 287

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 347

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 407

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 467

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||  ||||||
Db        468 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 527
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        528 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 587

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        588 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 647

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 698
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RESULT 7
US-10-312-245-7
; Sequence 7, Application US/10312245
; Publication No. US20030219419A1
; GENERAL INFORMATION:
; APPLICANT: University of Louisville Research Foundation, Inc.
; APPLICANT: Shirwan, Haval
; TITLE OF INVENTION: Methods and Compositions for Altering Cell Membrane Function.
; FILE REFERENCE: 1160.015WO1
; CURRENT APPLICATION NUMBER: US/10/312,245
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/215,580
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SA-TNFa
US-10-312-245-7

Query Match 94.9%; Score 447; DB 7; Length 702;
Best Local Similarity 96.8%; Pred. No. 3e-116;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        158 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 217

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 277

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 337

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 397

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||  ||||||
Db        398 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 457

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        458 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 517

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        518 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 577

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        578 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 628
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RESULT 8
US-10-825-282-17
; Sequence 17, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
;  APPLICANT: 3921-1-1-1
;  TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
;  TITLE OF INVENTION:  METHODS FOR MAKING AND USING THE SAME
;  FILE REFERENCE: 3921-1-1-1
;  CURRENT APPLICATION NUMBER: US/10/825,282
;  CURRENT FILING DATE:  2004-04-14
;  PRIOR APPLICATION NUMBER: US/09/456,357
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: 60/134,416
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 09/087,195
;  PRIOR FILING DATE: 1998-05-29
;  PRIOR APPLICATION NUMBER: 08/378,507
;  PRIOR FILING DATE: 1995-01-26
;  PRIOR APPLICATION NUMBER: 08/250,478
;  PRIOR FILING DATE: 1994-05-27
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 702
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(702)
US-10-825-282-17

  Query Match             94.9%;  Score 447;  DB 9;  Length 702;
  Best Local Similarity   96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||   |||||||||||||||||||   ||||||
Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 9
US-10-157-305A-19
; Sequence 19, Application US/10157305A
; Publication No. US20030166099A1
; GENERAL INFORMATION:
;  APPLICANT: Sabbadini, Roger A.
;  APPLICANT:  Surber, Mark W.
;  APPLICANT:  Neil Berkley
;  APPLICANT:  Anca M. Segall
;  APPLICANT:  Robert Klepper
;  TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS
;  FILE REFERENCE: MPEX.008DV1
;  CURRENT APPLICATION NUMBER: US/10/157,305A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,566
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/154,951
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 258
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 780
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-157-305A-19

  Query Match             94.9%;  Score 447;  DB 7;  Length 780;
  Best Local Similarity   96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        256 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 315

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 375

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 435

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 495

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||   |||||||||||||||||||   ||||||
Db        496 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 555

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        556 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 615

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        616 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 675

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 726


RESULT 10
US-10-157-391-19
; Sequence 19, Application US/10157391
; Publication No. US20030166279A1
; GENERAL INFORMATION:
;  APPLICANT: Sabbadini, Roger A.
;  APPLICANT:  Neil Berkley
;  TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
;  FILE REFERENCE: MPEX.008DV14
;  CURRENT APPLICATION NUMBER: US/10/157,391
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,566
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;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/154,951
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 257
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 780
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-10-157-391-19

  Query Match             94.9%;  Score 447;  DB 7;  Length 780;
  Best Local Similarity   96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        256 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 315

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 375

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 435

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 495

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        556 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 615

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        616 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 675

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 726


RESULT 11
US-10-157-096-19
; Sequence 19, Application US/10157096
; Publication No. US20030190601A1
; GENERAL INFORMATION:
;  APPLICANT: Sabbadini, Roger A.
;  APPLICANT:  Neil Berkley
;  APPLICANT:  Surber, Mark W.
;  TITLE OF INVENTION: TARGET DISPLAY ON MINICELLS
;  FILE REFERENCE: MPEX.008DV12
;  CURRENT APPLICATION NUMBER: US/10/157,096
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,566
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/154,51
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 257
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 780
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-10-157-096-19

  Query Match             94.9%;  Score 447;  DB 7;  Length 780;
  Best Local Similarity   96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        256 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 315

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        316 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 375

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 435

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 495

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        496 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 555

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        556 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 615

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        616 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 675

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 726


RESULT 12
US-10-157-302-19
; Sequence 19, Application US/10157302
; Publication No. US20030190683A1
; GENERAL INFORMATION:
;  APPLICANT: Sabbadini, Roger A.
;  APPLICANT:  Surber, Mark W.
;  TITLE OF INVENTION: MINICELL-BASED RATIONAL DRUG DESIGN
;  FILE REFERENCE: MPEX.008DV17
;  CURRENT APPLICATION NUMBER: US/10/157,302
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/293,566
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/154,951
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 257
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 780
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-10-157-302-19

  Query Match             94.9%;  Score 447;  DB 7;  Length 780;
  Best Local Similarity   96.8%;  Pred. No. 3e-116;
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  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        256 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 315

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 375

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 435

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        436 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 495

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||||||||
Db        496 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 555

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        556 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 615

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        616 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 675

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 726


RESULT 13
US-10-157-215A-19
; Sequence 19, Application US/10157215A
; Publication No. US20030190749A1
; GENERAL INFORMATION:
;  APPLICANT: Surber, Mark W.
;  APPLICANT:  Sabbadini, Roger A.
;  APPLICANT:  Segall, Anca M.
;  APPLICANT:  Berkley, Neil
;  TITLE OF INVENTION: MINICELL-PRODUCING PARENT CELLS
;  FILE REFERENCE: MPEX.008DV23
;  CURRENT APPLICATION NUMBER: US/10/157,215A
;  CURRENT FILING DATE:  2002-05-28
;  PRIOR APPLICATION NUMBER: 60/293,566
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/154,951
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 258
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 780
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-157-215A-19

  Query Match             94.9%;  Score 447;  DB 7;  Length 780;
  Best Local Similarity   96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        256 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 315

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 375

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 435

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 495

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||||||||
Db        496 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 555

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        556 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 615

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        616 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 675

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 726


RESULT 14
US-10-157-299-19
; Sequence 19, Application US/10157299
; Publication No. US20030194714A1
; GENERAL INFORMATION:
;  APPLICANT: Sabbadini, Roger A.
;  APPLICANT:  Neil Berkley
;  APPLICANT:  Surber, Mark W.
;  TITLE OF INVENTION: MINICELL-BASED TRANSFORMATION
;  FILE REFERENCE: MPEX.008DV15
;  CURRENT APPLICATION NUMBER: US/10/157,299
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/293,566
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/154,951
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 257
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 780
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-10-157-299-19

  Query Match             94.9%;  Score 447;  DB 7;  Length 780;
  Best Local Similarity   96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        256 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 315

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        316 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 375

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        376 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 435

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        676 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 726
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RESULT 15
US-10-154-951B-19
; Sequence 19, Application US/10154951B
; Publication No. US20030194798A1
; GENERAL INFORMATION:
;  APPLICANT: Surber, Mark W.
;  APPLICANT:  Sabbadini, Roger A.
;  TITLE OF INVENTION: MINICELL COMPOSITIONS AND METHODS
;  FILE REFERENCE: MPEX.008A
;  CURRENT APPLICATION NUMBER: US/10/154,951B
;  CURRENT FILING DATE:  2002-05-24
;  PRIOR APPLICATION NUMBER: 60/293,566
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/359,843
;  PRIOR FILING DATE: 2002-02-25
;  NUMBER OF SEQ ID NOS: 258
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 780
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-154-951B-19

  Query Match            94.9%;  Score 447;  DB 7;  Length 780;
  Best Local Similarity  96.8%;  Pred. No. 3e-116;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        256 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 315

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        376 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 435

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 495

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        616 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 675
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Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        676 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 726
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GenCore version 5.1.9

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	447	94.9	699	2	US-08-394-600B-1	Sequence 1, Appli
3	447	94.9	699	2	US-08-889-909A-1	Sequence 1, Appli
4	447	94.9	699	2	US-08-230-428B-1	Sequence 1, Appli
5	447	94.9	699	3	US-09-156-163A-1	Sequence 1, Appli
6	447	94.9	699	3	US-09-982-308B-1	Sequence 1, Appli
7	447	94.9	699	3	US-08-395-456C-1	Sequence 1, Appli
8	447	94.9	699	3	US-08-487-453A-1	Sequence 1, Appli
9	447	94.9	699	7	PCT-US95-02513-1	Sequence 1, Appli
10	447	94.9	699	10	5422425-1	Patent No. 5422425
11	447	94.9	900	2	US-08-323-445A-9	Sequence 9, Appli
12	447	94.9	900	2	US-08-515-903A-9	Sequence 9, Appli
13	447	94.9	900	7	PCT-US95-12840-9	Sequence 9, Appli
14	447	94.9	947	2	US-08-184-009-89	Sequence 89, Appl
15	447	94.9	947	2	US-08-458-356-89	Sequence 89, Appl
16	447	94.9	947	3	US-08-460-736-89	Sequence 89, Appl
17	447	94.9	947	3	US-09-535-370-89	Sequence 89, Appl
18	447	94.9	947	3	US-09-663-667-89	Sequence 89, Appl
19	447	94.9	965	2	US-08-184-009-79	Sequence 79, Appl
20	447	94.9	965	2	US-08-458-356-79	Sequence 79, Appl
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23	447	94.9	965	3	US-09-663-667-79	Sequence 79, Appl
24	447	94.9	1324	5	US-09-543-679A-2652	Sequence 2652, Ap
25	447	94.9	1585	3	US-09-023-655-1329	Sequence 1329, Ap
26	447	94.9	1587	3	US-09-949-016-5156	Sequence 5156, Ap
27	447	94.9	1643	3	US-08-880-342-36	Sequence 36, Appl
28	447	94.9	1643	3	US-09-505-250-4	Sequence 4, Appli
29	447	94.9	2088	3	US-09-973-850-1	Sequence 1, Appli
30	447	94.9	2088	3	US-09-973-850-2	Sequence 2, Appli
31	447	94.9	2088	3	US-09-973-850-3	Sequence 3, Appli
32	447	94.9	5042	3	US-09-915-815-20	Sequence 20, Appl
33	447	94.9	5042	3	US-09-915-815-21	Sequence 21, Appl
c 34	447	94.9	10728	3	US-09-376-774-5	Sequence 5, Appli
35	447	94.9	17634	5	US-09-543-679A-2654	Sequence 2654, Ap
36	447	94.9	32798	3	US-09-604-694B-1	Sequence 1, Appli
37	445.4	94.6	471	2	US-08-538-875-2	Sequence 2, Appli
38	443.8	94.2	3977	2	US-07-794-400-2	Sequence 2, Appli
39	443.8	94.2	3977	2	US-08-041-648-1	Sequence 1, Appli
40	443.8	94.2	3977	2	US-08-217-529-1	Sequence 1, Appli
41	443.8	94.2	3977	2	US-08-397-470-2	Sequence 2, Appli
42	441	93.6	465	3	US-09-604-694B-2	Sequence 2, Appli
43	440.6	93.5	935	10	5182196-3	Patent No. 5182196
44	434.8	92.3	3977	2	US-07-794-400-13	Sequence 13, Appl
45	434.8	92.3	3977	2	US-08-397-470-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
5182196-1
;Patent No. 5182196
; APPLICANT: ALLET, BERNARD;KAWASHIMA, ERIC H.
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR OVERPRODUCTION OF
;DESIRED PROTEINS
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,281
; FILING DATE: 27-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 53,398
; FILING DATE: 18-MAY-1987
; APPLICATION NUMBER: 785,847
; FILING DATE: 09-OCT-1985
;SEQ ID NO:1:
; LENGTH: 660
5182196-1

Query Match 94.9%; Score 447; DB 10; Length 660;
Best Local Similarity 96.8%; Pred. No. 3e-91;
Matches 456; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db        143 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 202

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        203 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 262

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 322

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        323 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 382

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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RESULT 2
US-08-394-600B-1
; Sequence 1, Application US/08394600B
; Patent No. 5843693
;  GENERAL INFORMATION:
;    APPLICANT:  Halenbeck, Robert F.
;    APPLICANT:  Jewell, David A.
;    APPLICANT:  Koths, Kirston E.
;    APPLICANT:  Kriegler, Michael
;    APPLICANT:  Perez, Carl
;    TITLE OF INVENTION:  Compositions for the Inhibition of
;    TITLE OF INVENTION:  Protein Hormone Formation and Uses Thereof
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street; 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/394,600B
;      FILING DATE:  02/27/95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Donald J. Pochopien
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  820.005/11850US05
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..699
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  229..699
US-08-394-600B-1

  Query Match             94.9%;  Score 447;  DB 2;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 3
US-08-889-909A-1
; Sequence 1, Application US/08889909A
; Patent No. 5853977
;  GENERAL INFORMATION:
;    APPLICANT:  Dalie, Barbara
;    APPLICANT:  Fan, Xuedong
;    APPLICANT:  Lundell, Daniel
;    APPLICANT:  Lunn, Charles
;    APPLICANT:  Tan, Jimmy
;    APPLICANT:  Zavodny, Paul
;    TITLE OF INVENTION:  Mammalian TNF-a Convertases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033-0530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/889,909A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,710
;      FILING DATE:  12-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dulak, No. 5853977man C.
;      REGISTRATION NUMBER:  31,608
;      REFERENCE/DOCKET NUMBER:  JB0601
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 298 2906
;      TELEFAX:  908 298 5388
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
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;      OTHER INFORMATION:  The residue at position -14 of the sequence
;      OTHER INFORMATION:  is a phenylanine in the Swiss-Prot sequence, Accession
;      OTHER INFORMATION:  Code Swiss-Prot P01375, and as a serine in the GenBank sequen
;      OTHER INFORMATION:  Accession Number M10988.
US-08-889-909A-1

  Query Match             94.9%;  Score 447;  DB 2;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 4
US-08-230-428B-1
; Sequence 1, Application US/08230428B
; Patent No. 5998378
;  GENERAL INFORMATION:
;    APPLICANT:  Kriegler, Michael
;    APPLICANT:  Perez, Carl
;    APPLICANT:  Halenbeck, Robert F.
;    APPLICANT:  Jewell, David A.
;    APPLICANT:  Koths, Kirston E.
;    TITLE OF INVENTION:  Compositions For The Inhibition Of TNF
;    TITLE OF INVENTION:  Hormone Formation And Uses Thereof (As Amended)
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION  Intellectual Property - R440
;      STREET:  4560 Horton Street, P.O. Box 8097
;      CITY:  Emeryville
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94662-8097
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/230,428B
;      FILING DATE:  19-APR-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,546
;      FILING DATE:  25-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/395,253
;      FILING DATE:  16-AUG-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Savereide, Paul B.
;      REGISTRATION NUMBER:  36,914
;      REFERENCE/DOCKET NUMBER:  0820.004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2718
;      TELEFAX:  (510) 655-3542
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..699
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  229..699
US-08-230-428B-1

  Query Match             94.9%;  Score 447;  DB 2;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

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Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 5
US-09-156-163A-1
; Sequence 1, Application US/09156163A
; Patent No. 6319681
;  GENERAL INFORMATION:
;    APPLICANT:  Dalie, Barbara
;    APPLICANT:  Fan, Xuedong
;    APPLICANT:  Lundell, Daniel
;    APPLICANT:  Lunn, Charles
```

```
;    APPLICANT:  Tan, Jimmy
;    APPLICANT:  Zavodny, Paul
;    TITLE OF INVENTION:  Mammalian TNF-a Convertases
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033-0530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 8.1
;      SOFTWARE:  Microsoft Word 6.0.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/156,163A
;      FILING DATE:  9/17/98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/889,909
;      FILING DATE:  July 10, 1997
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McLaughlin, Jaye P.
;      REGISTRATION NUMBER:  41,211
;      REFERENCE/DOCKET NUMBER:  JB0601QB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908 298 5056
;      TELEFAX:  908 298 5388
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      OTHER INFORMATION:  The residue at position -14 of the sequence
;      OTHER INFORMATION:  is a phenylanine in the Swiss-Prot sequence, Accession
;      OTHER INFORMATION:  Code Swiss-Prot P01375, and as a serine in the GenBank sequen
;      OTHER INFORMATION:  Accession Number M10988.
US-09-156-163A-1

  Query Match             94.9%;  Score 447;  DB 3;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 6
US-09-982-308B-1
; Sequence 1, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
;  APPLICANT: Dalie, Barbara
;  APPLICANT:  Fan, Xuedong
;  APPLICANT:  Lundell, Daniel
;  APPLICANT:  Lunn, Charles A.
;  APPLICANT:  Tan, Jimmy C.
;  APPLICANT:  Zavodny, Paul J.
;  TITLE OF INVENTION: Mammalian TNF-alpha Convertases
;  FILE REFERENCE: JB0601QC
;  CURRENT APPLICATION NUMBER: US/09/982,308B
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/156,163
;  PRIOR FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 08/889,909
;  PRIOR FILING DATE: 1997-07-10
;  PRIOR APPLICATION NUMBER: 60/021,710
;  PRIOR FILING DATE: 1996-07-12
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 699
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-982-308B-1

  Query Match             94.9%;  Score 447;  DB 3;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 7
US-08-395-456C-1
; Sequence 1, Application US/08395456C
; Patent No. 6586222
;  GENERAL INFORMATION:
;       APPLICANT: Halenbeck, Robert F.
;                  Jewell, David A.
;                  Koths, Kirston E.
;                  Kriegler, Michael
;                  Perez, Carl
;       TITLE OF INVENTION: Compositions for the Inhibition of
;                           Protein Hormone Formation and Uses Thereof
;       NUMBER OF SEQUENCES: 30
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy
;            STREET: 500 West Madison - 34th Floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: United States of America
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/395,456C
;            FILING DATE: 28-Feb-1995
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Pochopien, Donald J.
;            REGISTRATION NUMBER: 32,167
;            REFERENCE/DOCKET NUMBER: 0820.006/1296 11850US06
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/775-8000
;            TELEFAX: 312/775-8100
;            TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 699 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  1..699
;       FEATURE:
;            NAME/KEY:  mat_peptide
;            LOCATION:  229..699
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-395-456C-1

  Query Match             94.9%;  Score 447;  DB 3;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||
Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 8
US-08-487-453A-1
; Sequence 1, Application US/08487453A
; Patent No. 6599706
;  GENERAL INFORMATION:
;    APPLICANT:  Halenbeck, Robert F.
;    APPLICANT:  Jewell, David A.
;    APPLICANT:  Koths, Kirston E.
;    APPLICANT:  Kriegler, Michael
;    APPLICANT:  Perez, Carl
;    TITLE OF INVENTION:  Recombinant PR-3 and Assays Employing the Same
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,453A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien, Donald J.
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  27527/32753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..699
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  229..699
US-08-487-453A-1

  Query Match             94.9%;  Score 447;  DB 3;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
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  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 9
PCT-US95-02513-1
; Sequence 1, Application PC/TUS9502513
;  GENERAL INFORMATION:
;    APPLICANT:  Halenbeck, Robert F.
;    APPLICANT:  Jewell, David A.
;    APPLICANT:  Koths, Kirston E.
;    APPLICANT:  Kriegler, Michael
;    APPLICANT:  Perez, Carl
;    TITLE OF INVENTION:  Compositions for the Inhibition of
;    TITLE OF INVENTION:  Protein Hormone Formation and Uses Thereof
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02513
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams Jr., Joseph A.
;      REGISTRATION NUMBER:  38,659
;      REFERENCE/DOCKET NUMBER:  27527/32404
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  699 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..699
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  229..699
PCT-US95-02513-1

  Query Match             94.9%;  Score 447;  DB 7;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        649 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 699


RESULT 10
5422425-1
;Patent No. 5422425
;    APPLICANT: KRIEGLER, MICHAEL; NITECKI, DANUTE E.
;    TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF CYTOKINE
;CONVERTASE INHIBITORS
;    NUMBER OF SEQUENCES: 12
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/53,558
;      FILING DATE: 26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 562,720
;      FILING DATE: 06-AUG-1990
;SEQ ID NO:1:
;      LENGTH: 699
5422425-1

  Query Match             94.9%;  Score 447;  DB 10;  Length 699;
  Best Local Similarity   96.8%;  Pred. No. 3e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        229 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 288

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 348

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 408

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Db        409 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 468

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        469 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 528

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
                ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        529 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 588

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
                ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        589 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 648

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 11
US-08-323-445A-9
; Sequence 9, Application US/08323445A
; Patent No. 5763733
;  GENERAL INFORMATION:
;    APPLICANT:  Whitlow, Marc
;    APPLICANT:  Filpula, David
;    APPLICANT:  Shorr, Robert
;    TITLE OF INVENTION:  Antigen-Binding Fusion Proteins
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/323,445A
;      FILING DATE:  13-Oct-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bugaisky, Lawrence B.
;      REGISTRATION NUMBER:  35,086
;      REFERENCE/DOCKET NUMBER:  0977.2060000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  900 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  86..784
US-08-323-445A-9

  Query Match             94.9%;  Score 447;  DB 2;  Length 900;
  Best Local Similarity   96.8%;  Pred. No. 3.2e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
                ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        314 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 373

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 433

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 493

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
                ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        494 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 553

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
                ||||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||
Db        554 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 613

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
                ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        614 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 673

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
                ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        674 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 733

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 784
```

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RESULT 12
US-08-515-903A-9
; Sequence 9, Application US/08515903A
; Patent No. 5767260
;  GENERAL INFORMATION:
;    APPLICANT:  Whitlow, Marc
;    APPLICANT:  Filpula, David
;    APPLICANT:  Shorr, Robert
;    TITLE OF INVENTION:  Antigen-Binding Fusion Proteins
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/515,903A
;      FILING DATE:  16-AUG-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Jorge A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  0977.2060001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
```

```
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  900 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  86..784
US-08-515-903A-9

  Query Match             94.9%;  Score 447;  DB 2;  Length 900;
  Best Local Similarity   96.8%;  Pred. No. 3.2e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        314 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 373

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 433

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 493

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        494 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 553

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||
Db        554 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 613

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        614 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 673

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        674 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 733

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 784


RESULT 13
PCT-US95-12840-9
; Sequence 9, Application PC/TUS9512840
;  GENERAL INFORMATION:
;    APPLICANT:  ENZON, INC.
;    TITLE OF INVENTION:  Antigen-Binding Fusion Proteins
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12840
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/323,445
;      FILING DATE:  13-OCT-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldstein, Jorge A.
;      REGISTRATION NUMBER:  29,021
;      REFERENCE/DOCKET NUMBER:  0977.206PC00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  900 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  86..784
PCT-US95-12840-9

  Query Match             94.9%;  Score 447;  DB 7;  Length 900;
  Best Local Similarity   96.8%;  Pred. No. 3.2e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        314 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 373

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 433

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 493

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        494 CAGGTCCTCTTCAAGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 553

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              ||||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||
Db        554 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 613

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        614 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 673

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        674 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 733

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 784


RESULT 14
US-08-184-009-89
; Sequence 89, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
```

```
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10036
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/184,009
;       FILING DATE:  19-JAN-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Frommer, William S.
;       REGISTRATION NUMBER:  25,506
;       REFERENCE/DOCKET NUMBER:  454310-2530
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 840-3333
;       TELEFAX:  (212) 840-0712
;       TELEX:  425066CURTMS
;   INFORMATION FOR SEQ ID NO:  89:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  947 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-184-009-89

  Query Match             94.9%;  Score 447;  DB 2;  Length 947;
  Best Local Similarity   96.8%;  Pred. No. 3.2e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        413 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 472

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        473 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 532

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
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Db        533 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 592

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
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Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
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Db        713 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 772

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        773 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 832

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 883


RESULT 15
US-08-458-356-89
; Sequence 89, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  947 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-89

  Query Match             94.9%;  Score 447;  DB 2;  Length 947;
  Best Local Similarity   96.8%;  Pred. No. 3.2e-91;
  Matches  456;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
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Db        413 GTCAGATCATCTTCTCGAACCCCGAGTGACAAGCCTGTAGCCCATGTTGTAGCAAACCCT 472

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
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Db        473 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 532

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
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Db        653 AGCCGCATCGCCGTCTCCTACCAGACCAAGGTCAACCTCCTCTCTGCCATCAAGAGCCCC 712

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        713 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAAGCCCTGGTATGAGCCCATCTATCTG 772

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
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Db        773 GGAGGGGTCTTCCAGCTGGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 832

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
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Db        833 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 883
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Search completed: September 17, 2006, 22:28:49
Job time : 260 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: September 17, 2006, 20:23:05 ; Search time 707 Seconds
(without alignments)
4644.878 Million cell updates/sec

Title: US-10-668-178-14
Perfect score: 471
Sequence: 1 gtcagatcatcttctcgaac.....actttgggatcattgccctg 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	456.6	96.9	471	12	ADH10169	Adh10169 Human tum
4	456.6	96.9	471	14	AEB45418	Aeb45418 Human TNF
5	450.2	95.6	471	14	AEB45476	Aeb45476 TNF-R2 sp
6	450.2	95.6	471	14	AEB45447	Aeb45447 TNF-R1 sp
7	448.6	95.2	471	14	AEB45448	Aeb45448 TNF-R1 sp
8	448.6	95.2	471	14	AEB45446	Aeb45446 TNF-R1 sp
9	447	94.9	471	1	AAN60442	Aan60442 Sequence
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17	447	94.9	662	1	AAN60447	Aan60447 Plasmid 1
18	447	94.9	662	2	AAT15425	Aat15425 Plasmid 1
19	447	94.9	699	1	AAN60499	Aan60499 Sequence
20	447	94.9	699	2	AAQ11244	Aaq11244 Encodes 2
21	447	94.9	699	2	AAQ54497	Aaq54497 Sequence
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23	447	94.9	699	2	AAV73931	Aav73931 Human pro
24	447	94.9	699	6	ABX15852	Abx15852 cDNA enco
25	447	94.9	699	6	AAI71059	Aai71059 Human tum
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28	447	94.9	702	1	AAN91641	Aan91641 Tumour ne
29	447	94.9	702	2	AAQ75241	Aaq75241 Human tum
30	447	94.9	702	6	ABK12875	Abk12875 Chimeric
31	447	94.9	702	6	AAD45859	Aad45859 Human tum
32	447	94.9	702	12	ADM45815	Adm45815 Protein c
33	447	94.9	702	13	ADU22876	Adu22876 Human apo
34	447	94.9	702	14	ADV42620	Adv42620 Human psy
35	447	94.9	702	14	ADZ75567	Adz75567 Human tum
36	447	94.9	702	14	AEA14682	Aea14682 Human pro
37	447	94.9	702	14	AEA14774	Aea14774 Human pro
38	447	94.9	771	1	AAN50166	Aan50166 Sequence
39	447	94.9	780	1	AAN71311	Aan71311 Sequence
40	447	94.9	780	1	AAN81275	Aan81275 DNA encod
41	447	94.9	780	10	ADB89283	Adb89283 Expressio
42	447	94.9	780	10	ADC24630	Adc24630 Human tum
43	447	94.9	780	10	ADD67907	Add67907 Human tum
44	447	94.9	780	10	ADE10355	Ade10355 Minicell
45	447	94.9	780	10	ADE11534	Ade11534 Human tum

ALIGNMENTS

RESULT 1
AEB45419
ID AEB45419 standard; DNA; 471 BP.
XX
AC AEB45419;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human TNF DNA, SEQ ID No:3.
XX
KW tumor necrosis factor; TNF; TNF inhibitor; inflammation;
KW autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW vasotropic; cerebroprotective; dermatological; immunomodulator;
KW antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2005066206-A1.
XX
PD 21-JUL-2005.
XX
PF 05-JAN-2005; 2005WO-JP000032.
XX
PR 06-JAN-2004; 2004JP-00001427.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (MAYU/) MAYUMI T.
PA (TSUT/) TSUTSUMI Y.
PA (NAKA/) NAKAGAWA S.
XX
PI Mayumi T, Tsutsumi Y, Nakagawa S, Ohta T;
XX
DR WPI; 2005-506850/51.
XX
PT Novel tumor necrosis factor TNF mutant protein, useful for treating
PT and/or preventing diseases such as inflammation, and other diseases

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PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Disclosure; SEQ ID NO 3; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents human TNF DNA. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 471 BP; 85 A; 166 C; 127 G; 93 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 469.4;  DB 14;  Length 471;
  Best Local Similarity   99.8%;  Pred. No. 8.2e-87;
  Matches  470;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCGGGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 2
AEB45420
ID   AEB45420 standard; DNA; 471 BP.
XX
AC   AEB45420;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human TNF DNA, SEQ ID No:4.
XX
KW   tumor necrosis factor; TNF; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Disclosure; SEQ ID NO 4; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents human TNF DNA. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 471 BP; 86 A; 166 C; 126 G; 93 T; 0 U; 0 Other;

  Query Match             99.3%;  Score 467.8;  DB 14;  Length 471;
  Best Local Similarity   99.6%;  Pred. No. 1.7e-86;
  Matches  469;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCGACGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
```

RESULT 3
ADH10169
ID ADH10169 standard; DNA; 471 BP.
XX
AC ADH10169;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human tumour necrosis factor variant protein encoding DNA.
XX
KW TNF; tumour necrosis factor; polyethylene glycol; cytostatic; cancer;
KW human; variant; gene; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .471
FT   /*tag= a
FT   /product= "TNF variant"
FT   /partial
FT   /note= "the start and stop codons are not indicated"
XX
PN EP1354893-A2.
XX
PD 22-OCT-2003.
XX
PF 30-JAN-2003; 2003EP-00250587.
XX
PR 25-MAR-2002; 2002JP-00083509.
PR 26-JUN-2002; 2002JP-00185387.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (MAYU/) MAYUMI T.
PA (TSUT/) TSUTSUMI Y.
PA (NAKA/) NAKAGAWA S.
XX
PI Mayumi T, Tsutsumi Y, Nakagawa S, Ikegami H;
XX
DR WPI; 2004-063952/07.
DR P-PSDB; ADH10160.
XX
PT A physiologically active complex which comprises a protein part with
PT tumor necrosis factor activity and a high molecular part has higher
PT stability and retention in living bodies and is useful to treat disease,
PT particularly cancer.
XX
PS Example 1; SEQ ID NO 12; 18pp; English.
XX
CC The present sequence represents a physiologically active complex which
CC comprises a proteinaceous part with tumour necrosis factor (TNF) activity
CC and a high molecular part bound artificially to the N-terminus of the
CC proteinaceous part. The proteinaceous part comprises the sequence
CC selected from ADH10159 and the molecular part has a molecular weight of
CC 500-5000 Da and is a homopolymer of polyethylene glycol or a copolymer of
CC ethylene glycol and its derivatives. The invention is used to treat
CC susceptive disease, particularly cancer. The complex has a higher
CC stability and longer retention time in living bodies than intact tumour
CC necrosis factor. The present sequence represents a DNA encoding a human
CC TNF variant protein.
XX
SQ Sequence 471 BP; 87 A; 166 C; 125 G; 93 T; 0 U; 0 Other;

```
  Query Match             96.9%;  Score 456.6;  DB 12;  Length 471;
  Best Local Similarity   98.1%;  Pred. No. 3.4e-84;
  Matches  462;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||||| |||||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
```

RESULT 4
AEB45418
ID AEB45418 standard; DNA; 471 BP.
XX
AC AEB45418;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human TNF DNA, SEQ ID No:2.
XX
KW tumor necrosis factor; TNF; TNF inhibitor; inflammation;
KW autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW vasotropic; cerebroprotective; dermatological; immunomodulator;
KW antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW ds.
XX

```
OS   Homo sapiens.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Example 1; SEQ ID NO 2; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
CC   overexpression of TNF, such as autoimmune diseases, tumors (e.g. colon
CC   cancer, rectal cancer, uterine cancer, brain tumor, leukemia, lymphoma),
CC   Crohn's disease, rheumatoid arthritis, allergies, psoriasis, cachexia,
CC   transplant rejection, stroke, ischemia, restenosis, AIDS, severe acute
CC   respiratory syndrome (SARS), atherosclerosis, Behcet's disease, systemic
CC   lupus erythematosus, malaria, meningitis, hepatitis, Alzheimer's disease,
CC   etc. The TNF mutant proteins are highly stable in vivo. This sequence
CC   represents human TNF DNA. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 471 BP; 87 A; 166 C; 125 G; 93 T; 0 U; 0 Other;

  Query Match            96.9%;  Score 456.6;  DB 14;  Length 471;
  Best Local Similarity  98.1%;  Pred. No. 3.4e-84;
  Matches  462;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 GTCAGATCATCTTCTCGAACCCCGAGTGACGCGCCTGTAGCCCATGTTGTAGCAAACCCT 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db          1 GTCAGATCATCTTCTCGAACCCCGAGTGACATGCCTGTAGCCCATGTTGTAGCAAACCCT 60

Qy         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAGCTGAGGGGCAGCTCCAGTGGCTGAACCGCCGGGCCAATGCCCTCCTGGCCAATGGC 120

Qy        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGAGCTGAGAGATAACCAGCTGGTGGTGCCATCAGAGGGCCTGTACCTCATCTACTCC 180

Qy        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGGTCCTCTTCTCGGGCCAAGGCTGCCCCTCCACCCATGTGCTCCTCACCCACACCATC 240

Qy        241 AGCCGCATCGCCGTCTCCTACCAGACCCGCGTCAACCTCCTCTCTGCCATCGCCAGCCCC 300
              |||||||||||||||||||||||||| |||||||||||||||||  |||||||
Db        241 AGCCGCATCGCCGTCTCCTACCAGACCCCCGTCAACCTCCTCTCTGCCATCCGCAGCCCC 300

Qy        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCCTCCCCTGGTATGAGCCCATCTATCTG 360
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        301 TGCCAGAGGGAGACCCCAGAGGGGGCTGAGGCCAACCCCTGGTATGAGCCCATCTATCTG 360

Qy        361 GGAGGGGTCTTCCAGCTGGAGACCGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420
              |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db        361 GGAGGGGTCTTCCAGCTGGAGCCGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGAC 420

Qy        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TATCTCGACTTTGCCGAGTCTGGGCAGGTCTACTTTGGGATCATTGCCCTG 471


RESULT 5
AEB45476
ID   AEB45476 standard; DNA; 471 BP.
XX
AC   AEB45476;
XX
DT   22-SEP-2005  (first entry)
XX
DE   TNF-R2 specific human TNF-alpha mutant protein DNA, SEQ ID No:60.
XX
KW   tumor necrosis factor-alpha; TNF-alpha; TNF inhibitor; inflammation;
KW   autoimmune disease; tumor; transplant rejection; cardiovascular disease;
KW   acquired immune deficiency syndrome; severe acute respiratory syndrome;
KW   plasmodium infection; meningitis; hepatitis; Alzheimers disease;
KW   antiinflammatory; cytostatic; antirheumatic; antiarthritic; antiallergic;
KW   antipsoriatic; anti-HIV; antiarteriosclerotic; immunosuppressive;
KW   vasotropic; cerebroprotective; dermatological; immunomodulator;
KW   antimalarial; antibacterial; hepatotropic; neuroprotective; nootropic;
KW   mutant; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2005066206-A1.
XX
PD   21-JUL-2005.
XX
PF   05-JAN-2005; 2005WO-JP000032.
XX
PR   06-JAN-2004; 2004JP-00001427.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PA   (MAYU/) MAYUMI T.
PA   (TSUT/) TSUTSUMI Y.
PA   (NAKA/) NAKAGAWA S.
XX
PI   Mayumi T,  Tsutsumi Y,  Nakagawa S,  Ohta T;
XX
DR   WPI; 2005-506850/51.
DR   P-PSDB; AEB45453.
XX
PT   Novel tumor necrosis factor TNF mutant protein, useful for treating
PT   and/or preventing diseases such as inflammation, and other diseases
PT   caused by overexpression of TNF, such as autoimmune diseases, tumor,
PT   rheumatoid arthritis, allergy.
XX
PS   Example 1; SEQ ID NO 60; 34pp; Japanese.
XX
CC   The invention relates to tumor necrosis factor (TNF) mutant proteins,
CC   particularly tumor necrosis factor mutant proteins specific for TNF-R1 or
CC   TNF-R2 (SEQ ID Nos 19-22 and 37-59 respectively). The invention discloses
CC   a TNF mutant protein comprising an amino acid sequence derived from the
CC   human TNF-alpha protein (given as SEQ ID No: 1) by the substitution of
CC   one or more amino acid residues at 29, 31, 32, 145, 146 and 147 from the
CC   N-terminus, and amino acid residues at positions 84-89 by other amino
CC   acid residue(s). Also described are: (1) a TNF inhibitor comprising a TNF
CC   mutant protein; and (2) a TNF formulation comprising a TNF mutant
CC   protein. The TNF mutant proteins are useful for treating and/or
CC   preventing diseases such as inflammation, and other diseases caused by
```